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AY398790 3371 bp DNA linear GSS 15-DEC-2003 Homo sapiens THBS2 gene, VIRTUAL TRANSCRIPT, partial sequence, GADODIC SHYDEN SEGUENCE.	AY308790 AY398790 AY398790.1 GI:39754762 GSS. Homo sapiens (human)	Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3371) Niclas Community of Miclas Community of Micros Community of	Clark, A.G., Glanowski, S., Niellen, K., Inomas, F., Kurphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous	gene trios Science 302 (5652), 1960-1963 (2003) 14671302 2 (bases 1 to 3371)	Clark, A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
RESULT 1 AY398790 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE	AUTHORS	JOURNAL PUBMED REFERENCE	AUTHORS

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Submitted (16-NOV-2003) Celera Gen Sockille, MD 20850, USA This sequence was made by sequenci them based on alignment. Location/Qualifiers 1. 3371 /organism="Homo sapiens" /db zref="taxon:9606" /locus_tag="HCM0008"	199.2%; Score 3369.4; DB 29; Length 3371; Conservative 0; Mismatches 1; Indels 0; Gaps Arggrergageragerergerage 2; Length 3371; Arggrergagerergerergergerergerergererger	CAGACAAAAACACGACCTTCAACCTTTCAGTATCAGAACATCAACCGCAAGACCATT [AAGAAGGCTTCTTCCTCACGCCCAGCTCAAGCAGGACGCAAGTCCAGGGGCACGCTG AAGAAGGGGCTTCTTCCTCACGGCCCAGCTCAAGCAGGCAG	GCGGACACGCTGGATCTCACCTACTGGATTGACGGCACCCGGCATGTGGTCTCCCTGGAG	TACAGCTTGCACGTGGGGTGCGACCTCATAGACAGCTTCGCTCTGGAGGCCCTTCTAC GAGGACCTGCAAGGGCTGCGAAAGAGCCGAAAGAGT [CTAAGCAAGAAGGTTGCCAGCAAGGCCAGGAACTGAGATCAACGCCATCAGTGAGAACCTAACGAACAAGGGTTGCCAGCAAGGGCCAGGGAACTGAGGATTGCCAGCAAGGGCCAGGGAAGATTGCCAGCAAGGGCCAGGGGAACTGAGGAATCAACGCCATCAGTGAGAACACGAGAAGGGTTGCGCATGTTCACCACCGAGTACGTGGGCCCCAGCTCAGAGAACATGATCACAGAGACCCCAGGTCAGAGAACATGCTCAGAGAACATGGTCCAGAAGATCGAGAACATGGTCCAGAAGATCGAGAAGATCGAGAAGATGGGCCCAGGTCAGAAGATGGATCACAGAAGATGGAAGAAGATGGAAAGATGGTCCAGAAGATGATCAGAAAGATGGTCCAGAAGATCTAGATCCAGAAACATGGTCCAGAAGATCTAAAAAGATGGATCCAGAAACATGGTCCAGAAACATGATCCAGAAACATGGTCCAGAAACATGATCCACAGAACATGATCCACAGAAACATGATCCACAGAAACATGATCCACAGAACCACTCCAGAAAACATGATCCACAGAACCACTCCAGAAAACATGATCCACAAAAAAAA
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Mus musculus 10 days neonate cortex cDNA, KIKEN full-length
enriched library, clone:A830097L06 product:FHROMBOSPONDIN 1
PRECURSOR homolog [Mus musculus], full insert sequence.
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Hayashizaki,Y. full-length cDNA cloning

Carninci, P. and High-efficiency

REFERENCE AUTHORS TITLE

RESULT 4
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JOCUS
DEFINITION

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

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The FANDYM CORDSTILUM and the KIKEN Genome Exploration Research Analysis of the mouse transcriptome based on functional annotation droup phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Rukuda, S., Furuno, M., Hanagaki, T., Hara, A., Haraka, T., Hayatsu, N., Hiramcock, T., Hiracka, T., Hayatsu, M., Hayashida, K., Jahata, K., Androck, T., Miracan, T., Katoh, H., Kanai, M., Matsuyawa, T., Miracan, M., Match, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyawa, T., Miyazaki, A., Murata, M., Ohasto, N., Okazaki, Y., Saitch, R., Sakai, C., Sakazume, N., Sano, H., Saanki, D., Saitch, R., Saitch, H., Sakai, K., Sakazume, N., Sano, H., Saaaki, D., Shibata, K., Shinaqawa, A., Shiraki, T., Takeda, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y., Tagami, M., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Saitch, Muramatsu, M. and Hayashizaki, Y., Saitch, Muramatsu, M. and Hayashizaki, Y., Saitch, Muramatsu, M. and Chemical Research (RIKEN), Laboratory for Genome Submitted (16-APR-2022) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Genome George Criken, Go. Jp/, Tel:81-45-503-922, Fax:81-45-503-9216)

RIKEN Yokohama Institute; 17-22 Suehiro-cho, Tsurumi-ku, Yokohama Institute; 17-22 Suehiro-cho, Tsurumi-ku, Yokohama Institute; 17-22 Suehiro-cho, Tsurumi-ku, Yokohama Institute of Genome Exploration Research droup Encyclopedia Project of Genome Exploration Research in Ruse Cenome Genome George Criken, Go. Jp/, Tel:81-45-503-922, The Coation of Experimental Animal Research in Riken contributed to prepare mouse tissues

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues

Coation of Experimental Animal Research in Riken Contributed Research Coation Collection Collection Collection Coll
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishli,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kaniwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonada,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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/db_xref="RANTOM DB:A820097L06"
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/Note="THROMBOSPONDIN 1 PRECURSOR homolog [Mus musculus]
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0; Mismatches 1112;
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Fax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Center for Molecular Medhanisms in Disease Wellcome Trust/MRC building Addenbrookes Hespital Cambridge) whose
                                                                                      S dachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kaguwa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kodoo, S., Konno, H., Kowai, C., Mateuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sagabo, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
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/db_xref="Laxon:10090"
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llarity 69.9%; Pred. No. 5.6e-202;
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/strain="C57BL/6J"
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(base, 11 on 3412)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wang, G., Zheng, X.H., White, T.U., Sninsky, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submission Cargill, M.

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Sockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                      GAGCACCTGCGGAATGCACTGTGGCACACAGGAAACACCCCTGGCCAGGTGCGCACCTG
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Pred. No. 1.2e-193;
0; Mismatches 1243; Indels 114;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="THBS1"
/locus_tag="HCM2162"
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Best Local Similarity 61.2%;
Matches 2142; Conservative
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                       GACCTGGACGCCCCAACCTCAATCTGGTCTGCGCCACCAAGGCCACCTACCACTGC
                                                                2125 GACCTGGACGGCTGGCCTAATGAAACCTGGTGTGTGTGCCCAACGCAACCTACCACTGC
                                                                                                                                                             AAAAAGGACAACTGCCCCAACCTTCCCAACTCGGGGCAGGAAGACTATGACAAGGACGCG
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1224 TTTGTGGAAGGCGAATGCTGC	1207	1524 AACTCCCGGTGCCCGGATC				1834 GTGCAAGCCCGTAACCCC 2124 TGCAACTCTACCTGGGCCACTTC 1894 TGCAACTACCTGGGCCACTTC 2184 GCGGGGGACGGCTCATCTGC 2244 CTGGTCTGCGCCACTATCTGCCCCATCTCTCTGCCACTGGCATCATCTGCCCATCTCTCTC
	CCAACCTGATCCC 204 AGAAGGAGGCTTC 383 DAGAAAAGGGTTTC 264 CTTGGCTCTGGAG 443 CCTTGGCTCTGAG 324 DD DD CTTGGCTCTGAG 324 DD DD CTTGGCTCTGAG 324		623 504 683 564	624 3 803	923 923 983 864	AGTGTCGAATGATAACCAGTTTCT 1043
CTGGTCCTGCTGGCTCTGTGGGTGTGGCCCAGCACGCAAGCTGGTCACCAGGACAAAGAC [1]	GIGAAGGGCCCCGACCTTCCAGCCCAGCTTTCCGCATGGGAGATGCCAACCTGATCCCC CCGGTGAACGCAGATGACCTAGCAAGATCACCAAGATGCGGGAGAAGGAGGCTTC			AAGAGCGGAIGIACGIGGCCAAAGGCICTGCCAGAGAGAGTCACTICAGGGGT		AACCAGCTCAGCAAAACCTCAAGAG ACCACGCTGCAGACATCCGCAA ATTGGTGGCCTCCTAAGACATCCGCAA TTGAGCGCCTCCTAAGACAAGAA TTGAGCGCCTCCTAAGACAGAA TTGAGCGCCTCCTGGGTGGA AGGAAAACAAGAATCGGTGTGTGA ACCATTGCCACAAATCGCTGCCC
144 28 204 85 264	Db 145 GTGAAGGGC Oy 324 CCGGTGAAC Db 205 CCTGTGCCT Oy 384 TTCCTCACG Db 265 CTCTTCTG	444 325 504 385	564 445 624 505	Oy 684 GCGGAAAG Db 565 AGAGCTG Oy 744 TGCTTCAG Db 625 CAGNNNNN		Oy 984 GTCCTCGTGA Db 865 ACCATTGTGA QY 1044 TGGGAGCTC7 Db 925 GCCAATGAGG QY 1104 CGGTTCTTT Db 967 GTTCAGTAC QY 1164 AAATTTAAAA Db 1027 AACTCAGTTD

1146 1343 1206 1233 1523 1293 1583 1413 1763 1593 1883 1653 1943 2123 1953 2303 1283 1206 1403 ACACCCCCATCCGGCACGCCGCCTGGAGCCACTGGTCA 1463 rgaacgggaagccrgrgaaggggaagcgcgggagagccaaa 1353 SCCCAATCGATGGCCGCTGGAGCCCCTGGTCCCCCGTGGTCG 1643 1703 saddadddahacadaacdradcarcarcadaacaacccc 1473 kedacifecerredrehreradadadadecekenteredake 1533 ATGGCTGTTTATCCAACCCCTGCTTCCCGGGAGCCCAGTGC 1823 rreargadrigcaaagaagrectreargectrectreargeac 1713 CGTCGGGGTCGGCCTGGAAGCAGCCAAGACGGAAAAGCAA 2063 crecaceeareeaacccaceacrecaacaacaacaacaag 1893 CAGCGACCCCATGTACAAGTGCGAGTGCCAGACAGGCTAC 2183 scagagagacregacergaacergaceccaacercaar 2243 scegedadeacacadaccidaareacridecedaareadaac 2013 deactriaccacrideaaaaaddaraarrideeceaaccrieec 2073 2304 AATTCTGGGCAGGAAGACTTTGACAAGGACGGGATTGGCGATGCCTGTGATGATGATGACGAT 2363 reaccreteseagrigecaararcacaccearccercrec rgacaigtigetgaigtgaigtgaiceagaiccegcictgc Arggargccrgrccaarcccrgcrrrgccggcgrgaagrgr CTGGTCATGCGGCTCCTGCCCTGTGGGCTTCTTGGGCAAT recaccioneconociones PATGCAAGGACAGACACAACTGCCACAAGCACGCGGAG ATAGGGACCCCATGTACGGCTGCGAGTGCAAGCCTGGCTAC 1224 TTTGTGGAAGGCGAATGCTGCCTTCCTGCCTCCACTCGGTGGACGGTGAGGAGGGCTGG CCAGTGCTCCGTGACGTGTGGCTCTGGGACCCAGCAGAGA ------chádardaródadadchadadchadradra regegecaagaattecaaagggagtgeccgggagaccaaa sccccarcaardaagcrccaccarccardaac COGTOGGATCCGGGAGCGCACCCGGGTCTGCAACAGCCCT AGGCCTGCGTGGGGGATGTGCAGGAGCGTCAGATGTGCAAC scriciaaaaricriciaricaacaacaacaaaaaaa CACCTACCACTGCATCAAGGATAACTGCCCCCATCTGCCA srccircecidrogeceaecaecreracadacandacida crecrienteraceaecrereceariceaarcacritaaa CAGCAACACCTGCTTGGGGCCCTCCATCCAGACACGGGCT

	AY405254 Mus musculus THBS1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. AY405254 AY405254 AY405254 Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (house mouse) I (base I to 3340) I (base I to 3340) I (base I to 3340) Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Adams, M. D. A., Zheng, K.H., White, T.J., Sninsky, J.J., Adams, M. D. A., Zheng, K.H., White, T.J., Sninsky, J.J.,	ψ Cl	1 sal Similarit 2071; conse 270 GGGCCGG 84 GGCCAGG 330 AACGCAGG 144 CGGGATGGG
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	2604 GACCGGATGGTGGGGTGTGGGGATCACTGGACAACTGGTGGACGCCCTGGGTGGACCCT 2663 2374 GACACGATGGTGGGGGTTGGAGATCACTGTGACAATTGCCCCTGGTGACACTCGTGACCCT 2663 2374 GACACTGATGGGGTTGGGATTCAGTGTGACAATTGCCCCTTGGAACAACGATCGC 2433 2664 GACCGGACCGACGACAATGACCTTGTTGGGACCATTGGACCAACGACAACAACAACAACAACAACAACAACAACAA	ATTCCTGATGACAAGGACAACTGCAACTGCCCAATCCCGACCAACGAAAGGACTCTGAC GGTGATGACAAGGACTGCAAACTGCCCCAATCCCGACCAACACAACAGACTCTGAC GGTGATGACGAGACTGATATTGTAAAGATGATTTTGACAATGACAACTGCCAGATATT GGCGATGTGTGCTGCAAACAATGACTTCAGGACACTTCCAGATG GATGACTTTTGACAAACAATTGACATCAGGACACTTCAGGAACTTCCAGATG GATGACATCTGTCCTGAAAACAAATTGACATCAGAACTTCCAGATG GATGACATCTGTCCTGAAAAACAATTGACATCCAAATTCCGCCGATTCCAGATG ATTCCTTTGGACAAAAGGGACACCCAAAATTGATCCCAAATGACGCTTTCAGGACTTCAGAACTCGACGAGGACACAAATTGACCCCAAAATGACACCCAAAATGACACCCGAAATTGACCCCAAAATGACTCGTTAGGTTTTGACCACAGACACAGACTCGTAGAAAAAAAA	

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204 TIGGCTICCTICAGGCAGATGAAGACCCGGGGCACACICCTGGCTGTGGAACGGAAA 263	450 GGTCTCTCCCAGAGGCAGTTCGAGATCGTCCAACGGCCCCGCGGACACGCGTGGATCTC 509	ACCTACTGGATTGACGGCACCCGGCATGTGGTCTCCCTGGAGGCGTCGCCTGGCTGG	AGCCIGAGCCIGCCAGGGAACAACAAGIGGICAGIGAAGAAGCICICCTGGGCCACTTGGCCACTTGGAAGAAGCICTGGCCAGTGGGGGGGGGG	384 GGCCAGTGGAAGAGCATCACGCTGTTGTTCAAGAGGAACCGGGCTCAACTCTACATAGAC 443 630 TGCGACCTCATAGACATCGCTCTGGACGAGGCCCTTCTACGAGCAGCAGCAGCAGA 689 644 TGCGACCTCATAGACATCATCATCATCATCATCATCACAACTCAACAATCAACAA	AAGAGCCGGATGTGCGAGGCTCTGCCAGAGAGAGTCATTCAGGGGTTTGCTT	CTGGCCAGCGTTGCCAGGCTCCGAGGTTGCAAAGGGAGATGTCAATGACAATTTTTCGNNN CAGAACGTCCACCTAGTGTTTGAAAACTCTGTGGAAGATATTCTAAGGAAGAAGGGTTGC	564 NHNININININININININININININININININININ		AGCCCTGCTATCCGCACCAACTACATCGGCCACAAAACAAAAGGACCTCCAAGCTATCTGT GAACGCTCGTGCGAGGAGGTGGGAAACATGGTCCAGGAGGTCTCGGGGGCTCCACGTCCTC	GECCTCTCCTGTGATGAACTATCCAGCATGGTCCTGGAACTGAAGGGCCTGCGCACCATC GTGAACCAGCTCAGCGAAACCTCAAGAGAGGTGTCGAATGATAACCAGTTTCTCTGGGAG	804 GIGACCACTCTGCAGGACAGCATCCGAAAAGIGACGGAAGAAGAAGAAGAGGTGGTGGTGAGT 863 1050 CTCATTGGTGGCCCTCCTAAGACAAGGAACATGTCAGCTGCTGGCAGGATGGCGGTTC 1109 664 GAGAGAAAGAAGAACATGTCAAGAAAAAAAAAAAAAAAA	TITGCGGAAAATGAAAGCGGGTGGGTGGAACAGCTGCACCACGTGTACCTGCAAGAATTT TATACAGAAAATGAAAACTGAACAGCTGCACCACGTGTACCTGCAAGAATTTT TACAAGAAAACGAGAGAGAGAAATTTTACAAGAAAAGAGAAGAGAGTGCAAGAAAAGAAAAAAAA		GAAGGCGAATGCTGCCCTTCCTGCCTCCACTCGGTGGACGGTGAGGGCTGGTTCTCCC	Tegecaagreerserserserserserserserserserserserser	TGGTCTGAGTGGACCTCCTGCTGCCGCACATGTGGGAATTCGGCTTAAA 113 TCCTGTGAGGTCACCAGCAACACCTGCTTGGGGGCCTCCATCCA	1410 CTGAGCAAGTGTGACACCGGCAGGACGCGCTGGAGCCACTGGTCACCTTGG	

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Inbrary, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor Technologies."
                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;

Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;

Mammalia, Eutheria; Primates; Catarrhini, Hominidae; Homo.

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mutional Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Prayed by: The I.M.A.G.E. Consortium

CDNA Library Prayed by: The I.M.A.G.E. Consortium

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 686.

High quality sequence stop: 686.

I.coation/Qualifiers

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                                        AGENCOURT 8744271 Lupski sciatic_nerve Homo sapiens cDNA clone IMAGE:6205936 5', mRNA sequence.
BO933301 GI:22348684
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RESULT 8
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2610 GATGGTGACGGTGTGGGGGATCACTGTGACACTGCCCCCTGGTGCACACACCCTGACACAC
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                                                                                                                                    2670 ACCGACGTGGACAATGACCTTGTTGGGGACCAGTGTGACAACAACAAGACGAGACATGATGAC
                                                                                                                                                                                                         2730 GACGGCCACCAGAACAACCAGGACAACTGCCCCTACATCTCCAACGCCAACCAGGCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3270 CAGACCTACTGGGAGGACCAGCCCACGCGGGCCTATGGCTACTCCGGCGTGTCCCTCAAG
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5'-TCGACCACGCGTCCG-3' and
5'-TCGACCACGGTCGCGCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor Technologies."
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                                                                                    organism="Homo sapiens'
                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6200142"
ity sequence stop:
Location/Qualifiers
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Homo sapiens

ENKaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Homo sapiens

ENKaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.

I (bases 1 to 891)

INTH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

AL Contact: Robert Strauberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CONTACT: Dr. James R. Lupski

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://imaga.llnl.gov

Plate: LiAM13614 row: i column: 07
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AGENCOURT 8883081 Lupski sciatic_nerve Homo sapiens cDNA clone
IMAGE:6200142 5', mRNA sequence.
BQ925776.1 GI:22340807
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Oy 376 AGGCTTCTTCCTCAGGCCCAGCTCAAGCAGGCAAGTCCAGGGGCACGCTGTTGG 435 Db 241 AGGCTTCTTCCTCAGGCCCAAGCTCAAGCAGGCAAGTCCAGGGGCACGCTGTTGG 300 436 CTCTGAGGGGCCCGGCTCTTCCCCAAGGACGCAGTTCCAAGGCCCGCGG 495 Db 301 CTCTGGAGGGCCCGGTCTCCCCAGAGGCAGTTCCAAGGCCCCGCGG 360 Qy 496 ACACGCTGGATCTCCCCAGAGGCAGTTCGAGATCTCCAATGGCCCCGCGG 360 Qy 496 ACACGCTGGATCTCACCTACTGGATTGACGCACCCGGCATGTGGTCTCCCTGGAGGACG 555 Db 361 ACACGCTGGATCTCACCTACTGGATTGACGCCCCGGCATGTGGTCTCCCTGGAGGACG 555	121 TCGGCCTGGCTGCACTCGCAGTGCAAGAACGTCACCGTGCAGGCTGGCAGGCCTACA 421 TCGGCCTGGCTGCACTCGCAGTGCAAGAACGTCACGTGCAGGCTGGCT	721 916 916 939 939 939 1 001	SOURCE Homo sapiens (human) ORGANISM Homo sapiens sapiens Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metacoa; Chordata; Catarrhini; Hominidae; Homo. L (bases 1 to 778) Couract Cane Institute, Cancer Genome Anatomy Project (CGAP), TITLE TUMOR Gene Institute, Cancer Genome Anatomy Project (CGAP), COMMENT Contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. Contact: Robert Strausberg, Ph.D. Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of Orthospedics CONA Library preparation Dr. M. Bento Soares, University of Iowa CDNA Library Preparation Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-GoaresGullowa.edu The following repetitive elements were found in this CDNA.
	REFERENCE LI, W. B., Gruber, C., Jessee, J. and Polayes, D. TITLE FUll-leased Loop Comen. EXPERENCE LI, W. B., Gruber, C., Jessee, J. and Polayes, D. TITLE FUll-leased Loop Comen. EXTREMENTATION BX390187 EXTRACCESSION BX390187 EXTRACCESSION BX390187 EXTRACCESSION BX390187 EXTRACCESSION BX390187 EXTRACOR BX390187 CONTEXT COLLACT GENOSCOPE GONDENT CONTEXT: Genoscope EXTRACOR BX390187 EXTRACOR BX30018 EXTRACOR BX30018	Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. Contact : Feng Liang Email: filiang@lifetech.com URL: http://fullength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOBAGOO7ZF12_CSO0670_1. Location/Qualifiers 1. 896 / organism="Homo sapiens" / mol Lype="MRNA" / mol Lype="MRNA" / db xaref="csonocology sequence" / db xaref="csonocology sequence" / clone="csonocology sequence" / tissue Lype="NEUROBLASTOMA COT 25-NORMALIZED" / clone="lib="homo sapiens NEUROBLASTOMA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	Query Match 13.9%; Score 790.2; DB 13; Length 896; Best Local Similarity 97.0%; Pred. No. 3.1e-108; Aistones 31.e-108; Matches 835; Conservative 0; Mismatches 22; Indels 4; Gaps 3; 138 TGGAGGTGGTGGTGGTGGGGGGGGGGGGGGGGGGGGGG

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MENLATORIAN METAGORY, CATAININIA, Wentebrata, Enteleostomi,
Mammalia, Eutheria, Primetes, Catarrhini, Hominidae, Homo.

NOES INTERNACIAL MEDICAL IND.

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NAIL ORDAN General Ind. 2007

TOTAL INDEAT PREPARATION: M. Betto Scares, University of Iowa CONA Library Preparation: M. Betto Scares, University of Iowa CONA Library Preparation: M. Betto Scares, University of Iowa CONA Library Preparation: M. Betto Scares, University of Iowa CONA Library Preparation: M. Betto Scares, University of Iowa CONA Library Preparation: M. Betto Scares, University of Iowa CONA Library Preparation: M. Betto Scares, University of Iowa CONA Library Arrayed by: The Iowa, G. B. Conscrium (LLNL)

DNA Sequencing by: Agencourt Biosciance Corporation

Clane distribution: McC clone distribution information can be future in the Iowa MCC B. Conscrium/LLNL at:

High quality sequence scop: 644.

1. 7607

Ab Zref= Exacon: 8666"

Actanism="Homo sapiens"

Mol type="MRNH" MCC 220"

Alab host = ThMGS: 30077733"

Alab host = Th
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                                                                                                                                             ACACATTGCATTTTGATAAAATTAATTTTGTTTTCTTTGAGGTTGATCGTTGTGTTG 119
GITAATAGTCATCACATTTCTATGCCAAACAGGAACAATCCATAACTTTAGTCTTAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                763 bp mRNA linear ES:
AGENCOURT 16368996 NIH MGC_220 Homo sapiens cDNA clone
IMAGE:30707733 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                             5364 CGTTGGGATACTTCATTAAATGTAGCGACTGTCAACAGCG 5403
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Pred. No. 1.2e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CK000113.1 GI:38526147
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99.7%;
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Best Local Similarity
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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CK000113
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                                                                                                                                                                                                                                                                                                                                               /day stage="Adult"
//day stage="Adult"
//day stage="Adult"
//dab_host="D4hidb (Life Technologies)"
//dobne_lib="NCI CGAp_Chi"
//dobne_lib="NCI CGAp_Chi"
//dobne_lib="NCI CGAp_Chi"
//dobne_lib="NCI CGAp_Chi"
//dobne_lib="NCI CGAp_Chi is a cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Dobble stranded cDNA was ligated to an Eook I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the manner of the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the manner of the synthesis was the synthesis was the synthesis was the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the manner of the synthesis was the s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     778 TAATATTTAATGAGTGACTATAGAATGCAACTCCATTTACCAGTAACTTATTTTAAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGAAAATATGAGGCTTGATAATATTAGGTTGTCACGATGAAGCATGCTAGAAGCTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.3%; Score 760; DB 14; Length 7 100.0%; Pred. No. 1.1e-103; ative 0; Mismatches 0; Indels
                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNRM"
/db_xref="taxon:9606"
/clone="UT-H-EZO-bar-m-21-0-UI"
/tissue_type="Chondrosarcoma Grade II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-E20
TAG_SEQ=ATCTAATATG"
                   > (CAAA) n#Simple_repeat
                                                                                                                  ocation/Qualifiers
               sequence: 356-404, > (CA)
Seq primer: M13 FORWARD
POLYA=Yes.
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Best Local Similarity
Matches 760; Conserv
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/tissum_type="sciatic nerve"
/dev stage="adult, 70 yr"
/lab_host="bulbski sciatic nerve"
/lab_host="bulbski sciatic nerve"
/clone lib="Lupski sciatic nerve"
/clone lib="Lupski sciatic nerve"
/note="Vector: pCMV-SPORT6" (Life Technologies); Site_1:
Not1; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCACGCGCTCG-3' and
5'-GACTAGTTCTAGATCGCGGCCCCT(1S)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTATCTAGGCTTTGGTAACTGCGACAAGTTGCTTTTACCTGATTTGATGATACATTTCA 4616
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://limage.lln.gov
Plate: LLANU3621 row: i column: 13
High quality sequence stop: 613.
Location/Qualifiers
I. 937
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="InASE:6202836"
/sex="male"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 AAAACAGTTACAAAATAAACGAACTCTCCTTTGTCCTACAATGAAAGCCCTCATGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GCTAAATAAATTATAAACAAGGGTCAATTCAAATTTGAAGTAATGTTTTAGTAAGGAGAG
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es 751; Conserv
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Best Local S:
Matches 751
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I (bases 1 to 937)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Tissue Procurement: James Martin
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this CDNA
sequence: 637-685, >(CAAA)n#Simple_repeat
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 904)

NIH-MGC http://mgc.ndi.nih.gov/.

NITH-MGC http://mgc.ndi.nih.gov/.

Inpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ArCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Http://mage-llh.gov/

Plate: LLGW2558 row: f column: 23

High quality sequence stop: 551.
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/db xref="taxon:960"
/clone="thARGE:6376342"
/clone="type="normal pigmented retinal epithelium"
/lab host="mBLOB (phage-resistant)"
/clone=lib="NIH_MGC_43"
/clone="topan: eye," Vector: poTB7; Site_1: Xho1; Site_2:
/clone='crgan: eye, Vector: poTB7; Site_1: Xho1; Site_2:
/cloned into EcoRI/Xho1 sites using the following 5;
adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using AP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |
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AGENCOURT_8784556 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6376342
5', mRNA sequence.
BQ940133
BQ940133.1 GI:22355611
EST.
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                           GTATCTAGGCTTTGGTAACTGCGGACAAGTTGCTTTTACCTGATTTGATGATACATTTCA
                                                                                                                    TTAAGGTTCCAGTTATAAATATTTTGTTAATATTTTATTAAGTGACTATAGAATGCAACTC
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12.9%; Score 736; DB 13; Length 904; 99.6%; Pred. No. 3.9e-100; ive 0; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                               4778
                                                                                                                                                                                                                                                                                                          721 AACAAACAICTAATAAGTATATAATCCCTGGTGAAATATGG 762
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/organism="Homo sapiens"
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 CACTITITACTITITGCGTGTGGAGCTGTATTCCCGAGACCAACGAAGCGTTGGGATAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_LIB=UI-H-FH1
TAG_SEQ=AGAATCCGGC"
                                                                                    ocation/Qualifiers
Seq primer: M13 FORWARD POLYA=Yes.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Dickson, Math. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505594.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg, R.
Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadana@systemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                      TCAGATCCATTCTGAAAAGCATGGGCATGGAGGACGCCTTCAACAAGGGACGGCCCAATT
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                               TGGCTGAAGATGAAGTTGAGGTATACATACCCCAGTTCAAATTAGAAGAGCATTATGAAC
                                              TGGCTGAAGATGAAGTTGAGGTATACATACCCCCAGTTCAAATTAGAAGAGCATTATGAAC
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98.8%; Score 1886; Di
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1900; Conservative 0; Mismatches Patent: EP 0278696-A2 1 17-AUG-1988;
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                                                                           GAGATGTTAGCATGTTCTTGTTGCTTCCAGATGAAATTGCCGATGTGCCACTGGCTTGG
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	ICTTGCTTCCAGATGAAATTGCCGATGTGCCCTGGCTTGGAGGCTGCTGGAAAGTGAAA ICTTGCTTCCAGATGAAATTGCCGATGTGCCCTGGCTTGGAGGCTGCTGGAAAGTGAAA ITACCTATGACAAACTCCAACAAGTGGACCACCAAAGCCAAATGGCTGGAAGTTG IAACCTATGACAACTCCAACAAGTGGACCAGCAAAATGGCTGAAGATGG IAACCTATGACAAACTCCAACAAGTGGACCACCAAAATGGCTGAAGATGG IAACCTATGACAAACTCCAACAAGTGGACCACCAAATGGCTGAAGATGGAAA IAACCTATGACACACCCAGTTCAAATTAGAAGAGCAATATGAACTCAGATCCATTCTGAGAA IAACCTATGACACACCCAGTTCAAATTAGAAGAGCAATATGACTCAGATCCATTCTGAGAA IAACCTATGACACACCAGTTCAAATTAGAAGAGCAATATGACTCAGATCCATTCTGAGAA IAACCTATGACACACAGAACTGTTCCACCAAAGCAAAATTCTCAGGAATAACAAAAAAAA	2009 AAIGGGAICAIGCCCAITIAGAITIICCIIACIAICAGIIIAIIIIIAIAAAIIAAAI

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| organism="Momo sapiens"
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| do xref="mRNA"
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| db xref="last mRNA"
| product="PAI mRNA"
| footo="plasminogen activator inhibitor"
| codon start="mRDLCVANTFAINLEKHLAKASPTQNLFLSPWSISSTWAMVYM|
| codon start="mRDLCVANTFAINLEKHLAKASPTQNLFLSPWSISSTWAMVXM|
| codon start="mRDLCVANTFAINLEKHLAKASPTQNLFLSPWSISSTWAMVXM|
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| codon start="mrDLCVANTFAINLERGHYSPRENTLUGGNUFLECTARD codor"
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a-PAI 75.1.
entry and computer-readable sequence for [1] kindly provided
D.Ye, 22-JAN-1987.
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inogen activator inhibitor; serine protease inhibitor.
saplens (human)
asplens (human)
las, Eutheria; Drimates; Catarrhini; Hominidae; Homo.
las, Eutheria; Primates; Catarrhini; Hominidae; Homo.
D., Wun, T.C. and Sadler, J.E.
cloning and expression in Escherichia coli of a plasminogen ator inhibitor from human placenta
ator inhibitor from human placenta
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bill Chem. 262 (8), 3718-3725 (1987)
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Webb.A.C.
Direct Submission
Submitted (12-JUN-1987) Andrew C. Webb, Department of Biological
Sciences, Wellesley, College, Wellesley, MA 02181, USA
Sciences, Wellesley, College, Wellesley, MA 02181, USA
PAI-2 is a member CC of the serine protease inhibitor (serpin)
Superfamily. It inhibits urokinase-type plasminogen activator. The
monocyte derived PAI-1.
Location/Qualifiers
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/ Organia="Homo sapiens"

/ Organia="Homo sapiens"

/ Mb_xref="taxon:9606"

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/ 3. 1320

/ notein product; PAI-2 precursor (AA -22 393)"
               Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                          Webb,A.C., Collins,K.L., Snyder,S.E., Alexander,S.J.,
Rosenwasser,L.J., Eddy,R.L., Shows,T.B. and Auron,P.E.
Human monocyte Arg-Serpin cDNA. Sequence, chromosomal assignment,
and homology to plasminogen activator-inhibitor
J. Exp. Med. 166 (1), 77-94 (1987)
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MIBOB2.1 GI:189562

Plasminogen activator inhibitor 2.

Homo sapiens (human)

SM Homo sapiens (human)

Homo sapiens (human)

Homo sapiens (human)

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mandalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Schleuning, W.D., Medcalf, R.L., Hession, C., Rothenbuhler, R., Shaw, A. and Kruthof, E.K.

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DD 1561 ACTITIACTITATIATITATIATIATAAAGAGAGTITITIAAATTATIATIGTGACTG 1620 OV 1635 COTATITIAATTAATTAATAAAGAAAGAAGAAGAAGAAGAAGAAGAAAA	1621 CCTATTTAATGTAATAAATAAGTTATAGAAGCAGATGATGTGTAATTTCCTATCTAAT 1695 AAATGCCTTTAATTGTTCTCATAATGAAGAATAAGTAAGT	1681 AATGCCTTTAATTGTTCTCATAATGAAGAATAAGTAGGTATCCCTCCATGCCCTTCTGT 1755 AATAAATACTGGAAAAAACATTAAACAATAGGGAAATATGTTATGTGCATTTCTAGA	Db 1741 AATAAATATCTGGAAAAACATTAAACAATAGGCAAATATATGTTATGTTATGTTTCTAGA 1800 Qy 1815 AATACATAACACATATATGTCTGTATCTTATATTCAATTGCAAGTATAAT 1868	RESULT 9 HUMPAI2A LOCUS HUMPAI2A LOCUS HUMPAIA 11near PRI 07-JAN-1995 DEFINITION Human plasminoden activator inhibitor mRNA, complete cds.	ACCESSION J03603 VERSTON J03603.1 GI:189546 KEYWORDS plasminogen activator inhibitor. SOURCE Homo sapiens (human)	ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AUTHORS Antalis, T.M., Clark, M.A., Barnes, T., Lehrbach, P.R., Devine, P.L., SChevzov, G., Goss, N.H., Stephens, R.W. and Tolstoshev, P. TITLE Cloning and expression of a CDNA coding for a human manner of the coding for a human activator inhibitor.	JOURNAL MICHOLYCE GEILVEG PIASMILLOSEN ACCIVACOL ILLIADICOL MICHOLYCE NACI. ACAG. Sci. U.S.A. 85 (4), 985-989 (1988) WEDLINE 88125032 PUBMED 3257578 COMMENT Colinary Cont. Human monocute cell line 11937 CHNA to mPNA	Clone BTA1445. Draft entry and printed copy of sequence for [1] kindly provious Annalis, 01/19/88. Polyadenylation signals are located a continuous and 17.11.	PEATURES FEATURES 1.1854 1.1854 Source 7.organism="Homo sapiens" 7.organism="Homo sapiens" 7.organism="Homo sapiens"	/mol_Cype="mkky" /mol_Cype="mkkyy" /map="1q23" /map="1q23" gene /	CDS /gene="CERIA" /gene="FCERIA" /note="Plasminogen activator inhibitor precursor"	/protein_id="AAA60004.1" /db_xref="G1:189547" /db_xref="G3:189547" /db_xref="G3:189547" /repolation="MFD1:VANTY:B21"	GSEGSTEDOMAKULOFNEUGANAVTPMTPENFTSCGFMOOLOKGSYPDAILOAQAADK GSEGSTEDOMAKULOFNEUGANAVTPMTPENFTSCGFMOOLOKGSYPDAILOAQAADK IHSSFRSLSSAINASTGNYLLESYNKLFGEKSASFREEYIRLOGKTYSSEFDAVDFLE CAREAKKINSWYKTQTKGKIPLILESCHOOLOTANVIAVYFKGKWKTPFEKKLNG I-VPFPVASAOPTPVOMWYI FRKI NIGYTEDIKAOILEI-PYAGDYSHILLI-PDEIADVS	TGLELLESEITYDKLNKWTSKDKMAEDEVEVYIPQFKLEEHYELRSILRSMGMEDAFN KGRANFSGMSERNDLFLSSVFHQAMYDVNBEGTEAAAGTGGVMTGRTGHGGPQFVADH PPLFLIMMKITNCILFFGRFSSP" mat pentide 52.1293	/gen /pro p upstrea	Query Match 96.8%; Score 1847.6; DB 9; Length 1854;
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                                                                                                           A16054 2409 bp RNA molecule with the activity of miniactivin. A16054.1 GI:512777
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Search completed: March 11, 2004, 03:36:22 Job time : 4868.51 secs

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Then invention relates to a new combination comprising 55 cDNAB (ADAZ489) - ADA24539) or their complements that end differentially regulated in an adipose sample. Also included are detecting differential expression of one or more cDNAs in a sample containing nucleic acids, screening several molecules or compounds to identify a ligand that specifically binds a cDNA, a vector comprising the cDNA, a host cell containing the vector, producing a protein, screening several molecules or compounds, producing
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an antibody and the isolated antibody. The cDNAs comprise sequences which are upregulated or downregulated in response to peroxisome proliferator-activated receptor gamma (PPARgamma) agonist. The combination comprising several cDNAs is useful for preparing a composition for diagnosing or treating diabetes mellitus, obesity, hypertension, atherosclerosis, cancer of the breast, prostate or colon, or polycystic ovarian syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
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colorectal carcinoma; ss.
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Pred. No. 0;
0; Mismatches 5; Indels 0)
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                                                                                  Human colon cancer antigen encoding cDNA SEQ ID NO:251,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA;
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Matches 1899; Conservative (
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03-NOV-1999;
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CTAAATAAAAACACAGAAATAATTAGACAATTGTCTATTATAACATGACAACCCTATTAA 1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of plasmid pcD-1214 cDNA 1900 bp insert encoding human precursor plasminogen activator inhibitor (PAI-2).
                                                                                     CTAAATAAAAACACAGAAATAATTAGACAATTGTCTATTATAACATGACAACCTTATTAA
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                                                                                                                       TITATAACATTAACTTTTACTTTGTTATTTATTTATATAATGGTGAGTTTTTAAAT
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                             TATTGCTCACTGCCTATTTAATGTAGCTAATAAAGTTATAGAAGCAGATGATCTGTTAAT
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73..138
139..130
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1456..1461
4.tag= 1577
4.tag= 1777
4.tag= 1777
1587..1609
7.tag= 177 rich repeat"
1597..1609
7.tag= 177 rich region"
1647..1653
7.tag= 187 rich region"
1647..1653
1661..1666
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Human precursor plasminogen activator inhibitor (PAI-2) having specified amino acid sequence and human mature PAI2 (23(5) to 415(P)) sequences are claimed. Fure DNA coding for human precursor PAI-2 and human mature PAI-2, a transfer vector pcD1214 as available in E. coli HB101 (pcD1214) (NRRL B-18161), transformed host cells (mammalian and yeast), and a method of culturing the transformed cells to produce PAI-2 are claimed. PAI-2 may have utility as a substitute for epsilon-aminocaproic acid (epsilon-ACA). The PAI-2 gene can be used as a probe to locate the gene coding for a PAI-2 or PAI-2-like activity. The PAI-2 can also be used to produce antibodies used in diagnostic assays. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAATGGAGGAGCATCTTTGTGTGGCAAACACACTCTTTGCCCTCAATTTATTCAAGCATCTGG
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                                                                                                                                                                                                                                                                                                                                                                                           Human precursor and mature plasminogen activator inhibitor - obtd. by recombinant techniques from lipo-polysaccharide-stimulated human monocytes.
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98.8%; Score 1886; DB 1; Length 1920;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1900; Conservative 0; Mismatches 5; Indels 1
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                                                                                                                                                                                                                                                               NEWE-) NEW ENGLAND MEDICAL CENT INC
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P-PSDB; AAP80473.
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311 GGTTCATGCAGCAGATCCAGAAGGGTAGTTATCCTGATGCGATTTTGCAGGCACAAGCTG 370 361 CAGATAAAATCCATTCATCCTTCCGCTCTCTGCATCTGAGTGATCCACAGGGA 420 11	ATGCTGTCTAAAGAAAGGGAAACTCCATTTGAGAAGAAACTAATTGGGCTTT		1021	1261 ATAAGATAACCAAGTGCATTTTATTTTTTTTTTTTTTTT

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                                                                                                                                               Deoxyribonucleic acid - encoding recombinant human plasminogen activator inhibitor, used for preventing conversion of plasminogen to plasmin.
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                                                                                                                                                                                                                 The sequence was obtd. from the combined sequences of lambda PAI-75.1 lambda PAI75.15, both isolated from a placental CDNA library. A recombinant vector contg. the DNA can be used to express PAI-2 which inhibits the conversion of plasminogen to plasmin and is used as an anticoagulant. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACATGGGCTCCAGGGCAGCACCGAAGACCAGATGGCCAAGGTGCTTCAGTTTAATGAA
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                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1885; Conservative 0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                          Sequence 1910 BP; 611 A; 382 C; 384 G; 533 T; 0 U; 0 Other;
                                                                                                                                                                                           English.
       87US-00097482
                                 (UNIW ) UNIV WASHINGTON (MONS ) MONSANTO CO.
                                                                                                                                                                                           Claim 1; Fig 4; 23pp;
                                                                                                        WPI; 1991-215146/29
P-PSDB; AAR13007.
                                                                             Wun TC;
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98.18; 99.78;

Query Match Best Local Similarity

Location/Qualifiers 49. .1296 /*tag= a

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Minactivin is produced by induced human monocytes, certain macrophages and transformed cells of monocytic lineage (see WO 86/01212). Using the AA sequence obtd. for peptides of minactivin, oligonucleotide probes can be syntheasleed, (see AAN70467- AAN70473, and AAN71181-N71183). The specific oligonucleotide probe may be radiolabelled and then used to screen cDNA libraries to identify clones contg. all or part of the minactivin gene. (Updated on 25-WAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                              DNA sequence encoding minactivin - used for monitoring and treating tumours and chronic inflammation such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2409 BP; 743 A; 500 C; 508 G; 658 T; 0 U; 0 Other;
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Tumour location, tumour inhibition, chronic inflammation; rheumatoid arthritis; ss.

Homo sapiens

Sequence encoding human minactivin.

(revised) (first entry)

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Db 1501 CTAAAATGGGATCATGCCCATTTAGATTTTCCTTACTATTATTTTTATAACATTA 1560 Qy 1575 ACTITTACTTTGTTATTTTTATATATAATGGTGAGTTTTTAAATTATT	RESULT 7 TAMN91177 standard; DNA; 2424 BP. XX AAN91177; XX AAN91177; XX XX AAN91177; Z-WAR-2003 (revised) DT 10-WAR-2003 (revised) XX XX XX Homo sapiens. XX XX DS 10-MA-1981 XX DS 3531797 PT 10-MA-1989. XX DS 10-MA-1989. XX XX XX XX XX XX DS -JUL-1987; 87DE-03722673. XX CON 10-1987; o be produced using recombinant DNA techniques. Pure PAI-2 can be produced in this way and has therapeutic uses. Antibodies to this protein can be considered to diagnose PAI-2 genetic defects. Patent no. DE-3713272 described CC used to diagnose PAI-2 genetic defects. Patent no. DE-3713272 described CC the 361 N-terminal AA's of this protein which are used here as probbes to CC rescreen the original cDNA bank, allowing the new sequence, encoding the CC entire PAI-2 mol.to be isolated. This PAI differs from human placental	
421 AGTGTCAATAAGCTGTTTGGTGAGAAGCTTCCGGGAAGAATATTCGACTC 480 495 TGTCAGAAATATTACTCCTCAGAACCCCAGGCAGTTCCGGGAAGAATATTCGACTC 480 491 TGTCAGAAAAAAGATTACTCCTCAGAACCCCAGGCAGTTGATTTTTTTT		1455 ACAGAAATAATTAGACAATTGTCTATTATAACATGACAACCCTATTAATCATTTGCTCTT 1514

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  PAI at posns. 120 (Asn replacing Asp), 404 (Asn replacing Lys), and (Ser replacing Cys). In addition Proline at posn. 393 is encoded by instead of CCG. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                            60;
                                                                      Query Match
91.7%; Score 1750; DB 1; Length 2424;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1823; Conservative 0; Mismatches 5; Indels 60.
                                                    Sequence 2424 BP; 723 A; 516 C; 533 G; 652 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA sequence encoding plasminogen activator inhibitor type 2 - and derived proteins and antibodies, useful therapeutically and in diagnosis.
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                                      Sequence encoding plasminogen activator inhibitor type 2 (PAI2) placental cDNA clone lambda-plc 1.
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Pred. No. 0;
0; Mismatches 5; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Table 1 Page 5; 6pp; German.
                                                                                         Protease inhibitor; thrombolytic; ss
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Best Local Similarity 99.7%;
Matches 1670; Conservative
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P-PSDB; AAP80058.
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1441 AGCAGATGATCTGTTAATTTCCTAATAAATGCCTTTAATTGTTCTCATAATGAAGA

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plasminogen activator inhibitor-2; PAI-2; inflammation treatment; cancer;
        TATATICAATIGCAAGIATAATAAATAAACCIGCTICCAAACAACAAAAATA 1899
                                                                                          Encodes Plasminogen Activator Inhibitor-2
                                                                                                                                     Location/Qualifiers
42. .1289
/*tag= a
/product= "PAI-2"
                                                                                                                                                                                                                                BIOTECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                        Example; Fig 1; 52pp; English
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                                              AAQ10849 standard; DNA; 1412
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                                                                                                                                                                                                                                              Steven J;
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P-PSDB; AAR10921.
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Prepn. of plasminogen activator inhibitor-2 - by fermentation of a fungal cell transformed with a genetic construct which expresses the plasminogen activator inhibitor-2.
                                                                                                                                                                                                                                                                                                                                          A lambda gt11 cDNA library constructed from phorbol-12-myristate-13-acetate stimulated cells of the human monocyte-11ke historytic lymphoma cell line 1937 was screened. (See AAQ10850 and AAQ1081 for the probe sequences). From the putative positive clones, one was selected (lambda gt11-186) which appeared to contain the entire PAI-2 coding region. The insert was cloned in Mi3mp19 to give pDBP1 and was sequenced. (Updated on 25-MAR-2003 to correct PA field.)
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Query Match 73.7%; Score 1405.6; DB 2; Length 1412; Best Local Similarity 99.7%; Pred. No. 3.1e-281; Matches 1408; Conservative 0; Mismatches 4; Indels 0;
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                              Query Match
Best Local Similarity 95.3%; Pred. No. 1.3e-280;
Matches 1484; Conservative 0; Mismatches 4; Indels 69;
C; 324 G; 421 T; 0 U;
Sequence 1512 BP; 449 A; 318
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                                                                                                                                                                                                                                                                                       The variant has amino acids 74-96 deleted, It retains the biological activity while lacking protease sensitivity of native PAI-2. The variant is preped. by alteration of the DNA encoding PAI-2 and expression in hosts. The Hinfl-Pil segment spanning the protease sensitive site in PAI-2 was replaced by synthetic oligonucleotides with cohesive Hinfl and Patl ends, creating a variant PAI-2 in which amino acids 74-96 inclusive were deleted. See also AAQ11620. (Updated on 09-JAN-2003 to add missing S field.)
                                                                                                                                                                                                                       TATTTTTCGGCAGATTTTCCTCACCCTAAAACTAAGCGTGCTGCTTCTGCAAAAGATTTT 1320
  1081 ATGACCTGTTTCTTTCTGAAGTGTTCCACCAAGCCATGGTGGATGTGAATGAGAGGGGCA 1140
                                                                                                                               TATITITCGCCAGATITITCTCACCCTAAAACTAAGCGTGCTGCTTCTGCAAAAAATTTT
                                                                                                                                                                                                                                                              TGTAGATGAGCTGTGCCTCAGAATTGCTATTTCAAATTGCCAAAAATTTAGAGATGTT
                                         CTGAAGCAGCCGCTGGCACAGGAGGTGTTATGACAGGGAGAAACTGGACATGGAGGCCCAC
                                                                     CTGAAGCAGCCGCTGGCACAGGAGGTGTTATGACAGGGAGAACTGGACATGGAGGCCCAC
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to treat inflammatory diseases e.g. rheumatoid arthritis, ulcerative
colitis and psoriasis and fibrinolytic diseases.
                                                                                                                                                                                                                                                                                                                                    TICTACATATITCTGCTCTTCTGAACACTTC 1433
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/product= "PAI-2 variant"
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22. .1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAI-2; protease sensitive site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ11819 standard; DNA; 1512
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P-PSDB; AAR12143.
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18-SEP-1991
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AGATGTTAGCATGTTCTTGTTGCTTCCAGATGAAATTGCCGATGTGTCCACTGGCTTGGA 901
                                                                                  The variant has amino acids 66-98 deleted. It retains the biological activity while lacking protease sensitivity of native PAI-2. The variant is prepd. by alteration of the DNA encoding PAI-2 and expression in hosts. DNA sequences encoding amino acids 66-98 were deleted from PAI-2 using the PCR technique of site-directed mutagenesis by overlap extension. See also AAQ11619. (Updated on 09-JAN-2003 to add missing OS field.)
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Plasminogen activator inhibitor-2 variants with modified protease - to treat inflammatory diseases e.g. rheumatoid arthritis, ulcerative colitis and psoriasis and fibrinolytic diseases.
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                                                                                                                                                                                                                                         Length 1482;
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Pred. No. 7.4e-268;
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Best Local Similarity 93.3%;
Matches 1453; Conservative (
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                       CAGGGATGTCGGAGGAATGACCTGTTTCTTTCTGAAGTGTTCCACCAAGCCATGGT
                                         CTCAGGGATGTCGGAGAGGAATGACCTGTTTCTTTCTGAAGTGTTCCACCAAGCCATGGT
                                                                             GGATGTGAATGAGGAGGGCACTGAAGCAGCGGCTGGCACAGGAGGTGTTATGACAGGAG
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22. .1167
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/product= "PAI-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAI-2; protease sensitive site;
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P-PSDB; AAR12144.
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18-SEP-1991
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Addition of a signal sequence to PAI-2 not only facilitates secretion of the glycosylated 60 kD form of PAI-2 but also directs correct processing of the signal. The signal-contg. variant was constructed such that the artificial signal was fused to the NH2- terminal methionine of PAI-2. Correct cellular processing of this signal peptide should result in a mature PAI-2 molecule of 41s amino acids with Met at its NH2-terminus. See AAQ11129 for PAI-2 with the alpha-1-antitrypsin signal sequence.
                                                                                                                                                                                                          Prepn. of glycosylated plasminogen activator inhibitor-2 (PAI-2) diagnosis and treatment of tumours, and in treatment of immuno:suppressant conditions and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1328 BP; 377 A; 300 C; 317 G; 334 T; 0 U; 0 Other;
/*tag= b
/note= "synthetic-claim3"
                                                                                                                                                                                                                                                         Disclosure, Fig 7; 70pp; English.
                                                                                                     89AU-00006179.
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                                                                                                                                                  Whitfeld P, Richardson MA,
                                                                                                                             (BIOT-) BIOTECHN AUST PTY
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P-PSDB; AAR11352.
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Query Match 65.5%; Score 1249.4; DB 2; Length 1328; Best Local Similarity 99.5%; Pred. No. 6.6e-249; Matches 1253; Conservative 0; Mismatches 6; Indels 0;
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Plasminogen activator inhibitor; PAI-2; signal sequence; diagnosis; treatment; tumour; inflammation; secretion; ss.

/*tag= a /product= "preB-PAI-2" 15. .71 Location/Qualifiers 15. .1316

sig_peptide

Synthetic

PreA-plasminogen activator inhibitor-2 with signal sequence

(revised)
(first entry)

09-JAN-2003 06-JUN-1991

AAQ11128;

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/label= alpha-1-antitrypsin
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P-PSDB; AAR11353.
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treatment; tumour; inflammation; secretion; alpha-1-antitrypsin; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Addition of a signal sequence to PAI-2 not only facilitates secretion of the glycosylated 60 kD form of PAI-2 but also directs correct processing of the signal. The signal-contg. variant was constructed such that the human alph-1-antitrypsin signal was fused to PAI-2 without its NH2-terminal methionine. Correct cellular processing of this signal peptide should result in a macure PAI-2 molecule of 414 maino acids with Glu at its NH2-terminus. See AAQ11128 for PAI-2 with a synthetic signal sequence. (Updated on 09-JAN-2003 to add missing OS field.)
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                                                                                                                                                                                                                                                                                                                                              Prepn. of glycosylated plasminogen activator inhibitor-2 (PAI-2) diagnosis and treatment of tumours, and in treatment of immuno:suppressant conditions and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.4%; Pred. No. 1.5e-247;
Matches 1247; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1340 BP; 374 A; 307 C; 318 G; 341 T; 0 U; 0 Other;
                                                                                                                                                                                         Bunn CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 8; 70pp; English
89AU-00006179
                                                             89AU-00006179
                                                                                                                                                                                            Whitfeld P, Richardson MA,
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GCAAAATCCCAAACTTGTTACCTGAAGGTTCTGTAGATGGGGATACCAGGATGGTCCTGG 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A PAI-2 positive clone was isolated after screening a library (see AAQ21117-8). A BglII site was created at the 5' end of the gene to create a mutation in the third position of the second codon. A AlfII site was created at the 3' end to create mutations in the third position of the last codon and in the first base of the stop codon. A clone derived from this procedure was designated pDBP2. Two linkers were ligated with the BglII-AfIII PAI-2 gene fragment from pDBP2 into HindII + BAmHI digested milmpl9 to form pDBP3. See also AAQ21117-19 and AAQ21121-25. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                Antitumour molecules for treatment of neoplasms - comprises first region for binding to uPA receptor and second region for uPA inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 AAACAATGGAGGATCTTTGTGTGGCAAACACACTCTTTGCCCTCAATTTATTCAAGCATC
20 AAAAGATGGAAGATCTTTGTGTGGCAAACACACTCTTTGCCTCAATTTATTCAAGCATC
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Best Local Similarity 99.2%; Pred. No. 2.2e-247;
Matches 1248; Conservative 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 2; 57pp; English.
                                              90GB-00017083
                                                                                                                                                                                                       Courtney MG
                                                                                                                                                      (DELZ ) DELTA BIOTECH
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P-PSDB; AAR20797.
                                                                                                                                                                                                       Ballance DJ,
                                                 03-AUG-1990;
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                                                         CCAAACTTGTTACCTGAAGGTTCTGTAGATGGGATACCAGGATGGTCCTGGTGAATGCT
                                                                                                                              GTCTACTTCAAAGGAAAGTGGAAAACTCCATTTGAGAAGAAACTAAAATGGGCTTTAATCCT
                                                                                                                                                           GTCTACTTCAAAGGAAAGTGGAAAACTCCATTTGAGAAGAAACTAAATGGGCTTTATCCT
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                            CCAAACTTGTTACCTGAAGGTTCTGTAGATGGGGATACCAGGATGGTCCTGGTGAATGCT
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                          620 rgaargergreractreaaaggaaagregaaaacrecarrrgagaagaacraaarggge
                                                       TITATCCTTTCCGTGTAAACTCGGCTCAGCGCACACCTGTACAGATGATGTACTTGCGTG
                                                                            TTTATCCTTTCCGIGTAAACTCGGCTCAGCGCACACCTGTACAAGATGATGTACTTGCGTG
                                                                                                                   AAAAGCTAAACATTGGATACATAGAAGACCTAAAAGGCTCAGATTCTAGAACTCCCATATG
                                                                                                                                                                            CTGGAGATGTTAGCATGTTCTTGTTGCTTCCAGATGAAATTGCCGATGTGTCCACTGGCT
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ABZ83797 standard; cDNA; 1024 ABZ83797 ABZ83797

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relevant gene; toxicological response; gene; ss. Toxicologically relevant human nucleotide sequence #956 Toxicologically

WO2003016500-A2

16-AUG-2002; 2002WO-US026514

16-AUG-2001; 2001US-0313080P

(PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

Schmeiser K; Kier LD, Pickett GG, Adkins K, Dunn RT, Neft RE, Alen P;

WPI; 2003-268322/26

Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity.

Claim 1; Page 298; 455pp; English

The present invention describes a method (M1) for determining a toxicological response to an agent, which comprises comparing the expression profile of one or more human toxic response genes. to a reference gene expression profile indicative of toxicity, and so determining the presence of a toxic response to the agent. Also determining the presence of a toxic response to the agent. Also cermining the presence of a toxic response to the agent. Also from the genes corresponding to the partial sequences given in ABZ82842 to ABZ84764, or their fragments of at least 20 nucleotides, or homologues cresponse gene plays a role on toxic response pathways by determining the response gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of calls or a human subject to a known toxic pharmaceutical or industrial agent, comprising: (a) exposing cells to an agent or isolating the test gene expression profile of toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test comparing the test profile of toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test profile of the expression profile of that gene after exposure to other known toxic compounds. The methods are useful for exposure to other known toxic compounds. The methods are useful for toxic toxic toxic responses on a cellular, organized toxic response and ensured for toxic compounds and cellular, organic corresponding of drugs, pharmaceutical compounds and chemicals

Sequence 1024 BP; 313 A; 233 C; 234 G; 244 T; 0 U; 0 Other;

ô Gaps 0; Query Match
Best Local Similarity 99.5%; Pred. No. 3.3e-200;
Matches 1017; Conservative 0; Mismatches 5; Indels 0.

153 122 213 123 CCCCATGGAGCATCTCGTCCCACCATGGCCATGGTCTACATGGGCTCCAGGGGGCAGCACCG 182 6 62 3 ATTCCCCAGAGAACAACCAGATTGAACAATGGAGGATCTTTGTGTGGCAAACACACTCT 94 TIGCCCICAATITATICAAGCATCIGGCAAAAGCAAGCCCCCACCCAGAACCICTICCICT 63 Triccicrica Trita Trica a centra a centra a de contra 34 AATAACCAGAGAACAACCAGATTGAAACAATGGAGGATCTTTGTGTGGGCAAACACACTCT 154 CCCCATGGAGCATCTCGTCCACCATGGCCATGGTCTACATGGGCTCCAGGGGGAGCACCG ò à d à 셤 ઠ 엄

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            Query Match
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Sequence 1188, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: NUTTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER PHARMACEUTICALS, INC.
CITY: PALO ALTO
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GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCES: 1508
CORRESPONDENCE ADDRESS:
STREET: 3174 PORTER DRIVE
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                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUW TYEE: FIDOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                 PRILING DATE: HERBITH
PRILING DATE: HERBITH
CLASSIFICATION WUMBER: US/09/023,655
FILING DATE: HERBITH
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FILING DATE: HERBITH
FILING DATE: FILING DATE:
FILING DATE: FILING DATE:
FILING DATE: FILING DATE:
FILING DATE: TARENTIN:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: 94-0001 US
TELEPAN: (650) 855-055
TELEPAN: (650) 855-055
TELEPAN: (650) 845-4166
INPORMATION FOR SEQ ID NO: 1189:
SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
IMMEDIATE SOURCE:
LINEARY: GENBANK
CLONE: 9189546
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Best Local Similarity 99.8
Matches 1850; Conservative
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CALIFORNIA
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           CCTATTTAATGTAGCTAATAAAGTTATAGAAGCAGATGATCTGTTAATTTCCTATCTAAT
                                           1695 AAATGCCTTTAATTGTTCTCATAATGAAGAATAAGTAAGGTATCCCTCCATGCCCTTCTGT
                                                              AATACATAACACATATATATGTCTGTATCTTATATTCAATTGCAAGTATAAAT 1868
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                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLLOW & Lardher
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
COUNTRY: USA
COUNTRY: USA
COMPUTER: USA
COMPUTER: ELAPPY disk
COMPUTER: ELAPPY disk
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: FOLOS/MS-DOS
SOFTWARE: PAELONIN Release #1.0, Version #1.25
COMPUTER: TEADABLE FORM:
MEDIUM TYPE: FOLOS/MS-DOS
SOFTWARE: PAELONIN Release #1.0, Version #1.25
CUMRENT APPLICATION NUMBER: US/07/911,531
FILING DATE: 1992015
CUMRENT APPLICATION WUMBER: 29,768
FILING DATE: 29,768
REPERRAICA FORMY INFORMATION:
NAME: BENT, Stephen A.
RECASTRATION NUMBER: 29,768
REPERRAICA FOOKET INFORMATION:
TELEFHONE: (703)633-4109
TELEFHONE: (703)633-4109
TELEFAM: 299149
INFORMATION POR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2409 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPPICATION NUMBER: CAUDLE
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                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: STEPHENS, Ross
APPLICANT: GOLDER, Jeffrey
APPLICANT: ANTALLS, Toni M.
APPLICANT: CLARK, Michelle A.
APPLICANT: CLARK, Michelle A.
APPLICANT: CLARK, Michelle A.
APPLICANT: ENTRRACH, Philip R.
TITLE OF INVENTION: MINACTIVIN
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     RESULT 3
WS-07-211-531-18
; Sequence 18, Application US/07911531
; Patent No. 5422090
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LOCATION: 49..1296
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LOCATION:
US-07-911-531-18
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                                                                                1 GTCAGACAGCAACTCAGAGAATAACCAGAGAACAACCAGATTGAACAACAATGGAGGATCTT
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Best Local Similarity 99.8%; Pred. No. 0; Matches 1850; Conservative 0; Mismatches
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1 GTCAGACAGCAACTCAGAGAATAACCAGAGAACAACAACGAACTTGAAACAATGGAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 ACCCAGAACCTCTTCCTCTCCCCATGGAGCATCTCGTCCACCATGGCCATGGTCTACATG
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                                 COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/693,636A
FILING DATE: 19910430
CLASSIFICATION NUMBER: US 07/025,815
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 16786/155 CHAC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1847.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 899149
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGHT: 2409 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS; double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA to genomic RNA
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.8%;
Matches 1850; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 49..1296
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US-07-693-636A-18
  COUNTRY:
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APPLICANT: BARNES, Thomas M.
APPLICANT: CLARK, Michelle A.
APPLICANT: CLARK, Michelle A.
APPLICANT: DEVINE, Peter L.
APPLICANT: LEHRBACH, Philip R.
APPLICANT: LEHRBACH, Philip R.
TITLE OF INVENTION: RECOMBINANT PRODUCT NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEB: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: ALexandria
STATE: Virginia
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Sequence 18, Application US/07693636A
Parent No. 5426044
GENERAL INFORMATION:
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	795 TACATAGAAGACCTAAAGGCTCAGATTCTAGAACTCCCATATGCTGGAGATGTTAGCATG 854	915 GAAATAACCTATGACAAACTCAACAAGTGGACCAGCAAAGACAAAATGGCTGAAGATGAA 974 901 GAAATAACCTATGACAAACTCAACAAGTGGACCAGCAAAGACAAAATGGCTGAAGATGAA 960 975 GTTGAGGTATACATACACATTACAATTAGAAGAGCATTATGAACTCAATTCTG 1034 976 GTTGAGGTATACATACATCAATTAGAAGAGCATTATGAACTCAGATCCATTCTG 1034 961 GTTGAGGTATACATACCCCAGTTCAAATTAGAAGAGCATTATGAACTCAGATCCATTCTG 1020	1035 AAAAGGATGGGCATGGAGGACGCCTTCAACAAGGGACGGGCCAATTTCTCAGGGATGTCG 1094			95 AGAIGITTICTACATATTTCTGCTCTTCTGAACAACTTCTGCTACCCACTAAATAAA	1441 ACAGAATTATTAGACCATTTATAACATGCCAACCCTATTAATCATTGGTCTT 1500 1515 CTAAAATGGGATCATGCCCATTTAGATTTTCCTTACTACCAGTTATTTTTATAACATTA 1574 1501 CTAAAATGGGATCATGCCCATTTAGATTTTCCTTACTATCAGTTTTATTATAACATTA 1560 1575 ACTTTTACTTTGTTATTTATTATTATAATGGTGAGTTTTTAAATTATT

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                   1081 GAGAGGAATGACCTGTTTCTTGAAGTGTTCCACCAAGCCATGGTGGATGTGAATGAG
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US-07-768-286B-3
US-07-768-286B-3
Sequence 3, Application US/07768286B
Sequence 3, Application US/07768286B
Sequence 3, Application US/07768286B
Sequence 3, Application US/07768286B
APPLICANT: RICHARDSON, Michael A.
TITLE OF INVENTION: VARIANTS OF PAI-2
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: 3
CITY: Alexandria
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STREET: 1800 Diagonal Road, Suite 500
CONDTER: Viginia
MEDIUM TYPE: Floppy disk
COMPUTER: PREABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PREABLE FORM:
MEDIUM TYPE: PROPPY disk
COMPUTER: 19910-11
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU90/00603
FILING DATE: 20-DEC-1990
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                                                                                                                          Gaps
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                                                                                        DB 1; Length 1610;
LOCATION: 49..1296
OTHER INFORMATION: /product= "human plasminogen
OTHER INFORMATION: activator inhibitor type 2 protein"
                                                                                                                        5; Indels
                                                                                      84.0%; Score 1602; Di
99.7%; Pred. No. 0;
:ive 0; Mismatches
                                                                                          Query Match
Best Local Similarity 99.7
Matches 1605; Conservative
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1452 ITTTATAACAITAACITITACITIGITATITATTATTATATATAAAGGIGAGITITI 1508
                                                                                                                                                               1082 CTCAGGGATGTCGGAGAAATGACCTGTTTCTTTCTGAAGTGTTCCACCCAAGCCATGGT
                                                      GCTAAACATTGGATACATAGAAGACCTAAAAGGCTCAGATTCTAGAACTCCCATATGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 AATGGAGGATCITIGIGIGIGGGAAACACACTCITIGCCCTCAATTTATTCAAGGATCIGGC 80
                                                                                                                                                                                                                                                                                                                                                                                                       site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.5%; Score 1402.6; DB 1; Length 1512; Best Local Similarity 95.3%; Pred. No. 0; Marches 1484; Conservative 0; Mismatches 4; Indels 69; Gaps
                                                                                                                                                                                                                                                                                                                                 MAME/KEY: CDS

LOCATION: 22..1200

LOCATION: 22..1200

COTHER INFORMATION: /function="Product binds to other information" urokinase, tissue plasminogen activator";
COTHER INFORMATION: /function="Product binds to other information" (product="FAI-2 variant, protease sensitive s: OTHER INFORMATION: /emoved" (pries information: /evidence=EXPERIMENTAL OTHER INFORMATION: /note="Codes for human plasminogen activator other information: inhibitor type 2 protein in which amino acids" US-07-768-286B-3
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/157 CHAC
TELECOMMUNICATION INFORMATION:
TELEFAX: (703)836-9300
TELEFAX: (89149
TELEFAX: 89149
INFORMATION FOR SED ID 03:
SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: GUNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORANISM: HOMO SADIENS
CELL LINE: WORD
CELL LINE: U937
INMEDIATS SOURCE:
CELL LINE: U937
INMEDIATS SOURCE:
CLONE: BTA 1916
FEATURE:
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                                                                                                                   141 CATGGTCTACATGGGCTCCAGGGCACCCCAAGACCAGATGGCCAAGGTGCTTCAGTT 200
                                                                                                                                                                                                                                                                                                                                                             TAATGAAGTGGGAGCCAATGCAGTTACCCCCATGACTCCAGAGAACTTTACCAGCTGTGG 301
                                                                                                                                                                                                                                                      GITCATGCAGCAGATCCAGAAGGGTAGITAICCIGATGCGAITTITGCAGGCACAAGCTGC 361
122 AAAAGCAAGCCCCACCAGAACCTCTTCCTCTCCCCATGGAGCATCTCGTCCACCATGGC 181
                                                                                                                                                                                                                                                                                                                                    782 GCTAAACATTGGATACATAGAAGACCTAAAGGCTCAGATTCTAGAACTCCCATATGCTGG
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                         81 AAAAGCAAACCCCACCAAGAACCTCTTCCTCCCCATGGAGCATCTCGTCCACACATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 TTATTTACTGGAAAGTGTCATAAGCTGTTTGGTGAGAAGTCTGCGAGGTTCCGGGAAGA
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/function= "Product binds to
urokinase, tissue plasminogen activator"
/product= "PAI-2 variant, protease sensitive site
removed"
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//note= "Codes for human plasminogen activator
inhibitor type 2 protein in which amino acids 66
to 98 inclusive have been deleted."
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                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GOSS, Neil H.
APPLICANT: GOSS, Neil H.
APPLICANT: GOSS, Neil H.
TITLE OF INVENTION: VARIANTS OF PAI-2
NUMBER OF SEQUENCES: 21
CORRESSEDNDERSS:
ADDRESSEE: FOLCY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
CONTRY: Urginia
CONTRY: Urginia
CONTRY: ISO Diagonal Road, Suite 500
CITY: Alexandria
CONTRY: Proposition
COMPUTER: Ploppy disk
COMPUTER: EMPC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/768,286B
FILING DATE: 19911011
CLASSIFICATION NUMBER: PCT/AU90/00603
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 16786/157 CHAC
TELERCOMMUNICATION INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 16786/157 CHAC
TELERCOMMUNICATION INFORMATION:
TELERAC: (703)836-9000
TELERAX: (703)83-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.4%; Score 1342.6; 93.4%; Pred. No. 0; ive 0; Mismatches
                                           Sequence 5, Application US/07768286B
Patent No. 5444153
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TELEEX: 899149
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENOTH: 1482 base pairs
TVPE: NUCLEIC ACID
TVPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL LIFE.
CELL LINE: U937
IMMEDIATE SOURCE:
CLONE: BTA 1922
FEATURE:
NAME/KEY: CDS
LOCATION: 22..1170
IDENTIFICATION WETHOD: e
OTHER INFORMATION: \( \text{Line} \)
OTHER INFORMATION: \( \text{Line} \)
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CELL TYPE: Monocyte
CELL LINE: U937
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Best Local Similarity 93.4
Matches 1454; Conservative
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HYPOTHETICAL: NO
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HYPOTHETICAL: N
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ORIGINAL SOURCE
                         JS-07-768-286B-5
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FEATURE: Sig_peptide
| NAME/KEY: Sig_peptide
| LOCATION: 15..71
| COTHER INFORMATION: /pi
| US-07-679-0528-14
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                                                                                                                              GCCAAAATTTAGAGATGTTTTCTACATATTTCTGCTCTTCTGAACAACTTCTGCTACCC 1441
                                                                                                                                                                                                                                                                                                                              1362 ATCATTTGGTCTTCTAAAATGGGATCATGCCCATTTAGATTTTCCTTACTATCAGTTTAT 1421
                                                                                                                                                                                                     1242 GCCAAAARTTTAGAGATGTTTTCTACATATTTCTGCTCTTCTGAACAACTTCTGCTACCC 1301
                                                                                                                                                                                                                                    ACTABATABABACACAGABATAATTAGACAATTGTCTATTATAACATGACAACCCTATTA 1501
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                                                                                                                                                                                                                                                                                                                                                                                  TITIATAACATTAACTTTTACTTTGTTATTATTATTTTATAATGTGGGGTTTTT 1478
                                                                                                             1322 CTGCTTCTGCAAAAGATTTTTGTAGATGAGCTGTGTGCCTCAGAATTGCTATTTCAAATT
                                                                1122 TAAGATAACCAACTGCATTTTATTTTTCGGCAGATTTTCCTCACCCTAAAACTAAGGGTG
                 TAAGATAACCAAGTGCATTTTATTTTTCGGCAGATTTTTGCTCACCCTAAAACTAAGCGTG
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CLASSIFICATION NUMBER: 16786/147 CHAC

TELESTHOR/DOCKET NUMBER: 16786/147 CHAC

TELESTHOR/DOCKET NUMBER: 16786/147 CHAC

TELESTHORION INFORMATION:

TELESTHORION: (703) 836-9300

TELESTHORION: (703) 836-9300

TELESTHORION: (703) 836-9300

TELESTHORIOR CARRESTICS:

CREATER SEQUENCE: (703) 836-9300

TELESTHORIOR CALDER CALD

TYPE: NUCLEIC ACID

TYPE: NUCLEIC ACID

TYPE: NUCLEIC ACID

TYPE: NUCLEIC ACID
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US-07-679-052A-14
US-07-679-052A-14
Sequence 14, Application US/07679052A
Patent No. 5298400
GENERAL INFORMATION:
APPLICANT: WHITPELD, Peter L.
APPLICANT: RICHARDSON, Michael A.
APPLICANT: RICHARDSON, Michael A.
APPLICANT: BUNN, Clive L.
TITLE OF INVENTION: RECOMBINANT PRODUCT
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STRATE: Virginia
COUNTRY: USA
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NAME/KEY: CDS
LOCATION: 15..1319
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                                                                                                                      Gaps
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0
                                                                             Length 1328;
                                                                                                                  6; Indels
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/product= "Synthetic signal peptide"
                                                                          Query Match
Best Local Similarity 99.5%; Pred. No. 3.1e-293;
Matches 1253; Conservative 0; Mismatches 6;
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TGGCTGAAGATGAAGTTGAGGTATACATACCCCAGTTCAAATTAGAAGAGCATTATGAAC
                                                                                                                                                                                 1090 TCTCAGGGATGTCGAAGAATGACCTGTTTCTTTCTGAAGTGTTCCAAGCCATGG
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LOCATION: 15.86

OTHER INNERMATION: /product= "a-1-antitrypsin signal"
US-07-679-052A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIREE: 1 1800 Diagonal Road, Suite 500
CITY: Alexandria
COUNTRY: Use 1
COUNTRY: 1239
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BATENII Release #1.0, Version #1.25
SOFTWARE: Patenii Release #1.0, Version #1.25
SOFTWARE: Patenii Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/679,052A
FILING DATE: 1991056
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/147 CHAC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1003 (836-9300)
TELEFRAX: (703) 683-94109
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MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/07679052A
Sequence 16, Application US/07679052A
Patent No. 18294100:
GRNERAL INFORMATION:
APPLICANT: WHITFELD, Peter L.
APPLICANT: RICHARDSON, Michael A.
APPLICANT: BUNN, Clive L.
TITLE OF INVENTION: RECOMBINANT PRODUCT:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1800 Diagonal Road, Suite 500
                                                                                                                                                   TCTCAGGGATGTCGGAGGGAATGACCTGTTT
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1340 base pairs
TYPE: NUCLEIC ACID
STRANDEDNES: double
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LOCATION: 15..1331
FEATURE:
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 Length 1340;
Score 1246; DB 1; Length 1
Pred. No. 2e-292;
0; Mismatches 5; Indels
Query Match
Best Local Similarity 99.6%;
Matches 1249; Conservative
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APPLICANT: Hu, Yi
APPLICANT: Horis
APPLICANT: Nepomnichy, Boris
APPLICANT: Nepomnichy, Boris
APPLICANT: Nalke, D. Walke,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1161
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GGAGAGCAGGAATTCCCCAATCTGTCAGGAATACTTAGATGGTGTGATTTCAATTTTACCAC
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Patent No. 6583269
GENERAL INFORMATION:
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US-10-024-427-1
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GRERAL INFORMATION:
Parent No. 658269
GRERAL INFORMATION:
APPLICANT: Walke, D. Wade
TITLE OF INVENTION: No. 6583269el Human Protease Inhibitor and Polymuclectides EncodiFINE REPERENCE: LEX.0283.USA
CURRENT APPLICATION NUMBER: US/10/024,427
CURRENT APPLICATION NUMBER: US/26,287
FRIOR FILING DATE: 2001-12-18
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Pred. No. 4.4e-58;
0; Mismatches 565; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: CO.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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STATE: MA
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                                                                                                                                                                                                                                                                                                         123 AAAGCAAGCCCCACCCAGAACCTCTTCCTCTCCCCATGGAGCATCTCGTCCACCATGGCC 182
                                                                                                                                                                                                                                                                                                                                              61 AAAGATGATCGTCATAAAAACATATTTTTCTCTCCCTGAGCCTCTCAGCTGCCCTTGGT 120
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                                                                                                                                                                                                                                63 ATGGAGGATCTTTGTGTGGCAAACACACTCTTTGCCCTCAATTTATTCAAGCATCTGGCA
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                                                                                                                                                                                           Gaps
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                                                                                                                                                       Length 1278;
                                                                                                                                                   Query Match
14.4%; Score 274; DB 4; Length 12
Best Local Similarity 53.4%; Pred. No. 6.6e-57;
Matches 683; Conservative 0; Mismatches 565; Indels
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1278
                                                                        TYPE: DNA
ORGANISM: homo sapiens
IS-10-024-427-1
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                                                                                                          CAGTICAAATTAGAAGAGCATTATGAACTCAGATCCATTCTGAAAAGCATGGGCATGGAG 1052
901 AIGGIGGCCTGGAGGAGCTCAGAAAACATGTCAGAAGAATCGGTGGTCCTTCCCC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1081 TTGTCAAAAATTATCCACAAAACCTTTGTGGAGGTGGATGAAAACGGTACCCAGGCAGCT
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$:08-315-831A-12
$:08-315-831A
$:08-315-831A
Batent No. 5663299
GENERAL INFORMATION:
APPLICANT: Remold-0. Donnell, Eileen
TITLE OF INVENTION: Human Monocyte Elastase Inhibitor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,831A
FILING DATE: September 30, 1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Ave. CITY: Boston
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us-10-084-817-27.rni

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US-08-662-318-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAAATTGTCCACAAGTCATTTGTGGAAGTGAATGAAGAGGGAACAGAGGCGCCAGCTGC 1055
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                                                                                                                                                                                                                     216 GACTTICCATTICAATACACGGITGAAGGITCATTCAAGATICCAGAGICTGAATGCIGA 275
                                                                                                                                                                                                                                                                                                                                                 276 TATCAACAAACGTGGAGCGTCTTATATTCTGAAACTTGCTAATAGATTATATATGGAGAA 335
                                                                                                                                                                                                                                                                                                                                                                                             461 GTCTGCGAGCTTCCGGGAAGAATATATTCGACTCTGTCAGAAATATTACTCCTCAGAACC 520
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                                                                                                                                 DB 1; Length 1316;
                                                                                                                            Score 268.4; DB 1; Length
Pred. No. 1.5e-55;
0; Mismatches 436; Indels
OTHER INFORMATION: /codon_start= 49 FEATURE:
                                                                                                                            Query Match
Best Local Similarity 55.3%;
Matches 543; Conservative
                                           ) NAME/KEY; mat_peptide;
; LOCATION: 49..1185
US-08-315-831A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 GTCTGCGAGCTTCCGGGAAGAATATATTCGACTCTGTCAGAAATATTACTCCTCAGAACC 520
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                                                                                                                                                                                                                                    GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Human Monocyte Elastase Inhibitor

NUMBER OF SEQUENCES: 16

COURRESPONDENCE ADDRESS: 16

CONDESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Ave.

STREET: 600 Atlantic Ave.

CITY: Boston

STRATE: MA

COUNTRY: USA

CONPUTER FEDABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATION TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWAREN PAPPLICATION DATA:

APPLICATION NUMBER: US/08/662,318

FILING DATE: September 30, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Plumer, Elizabeth R. R.

NAME: Dumer, Elizabeth R. R.

NAME: Dumer, Elizabeth R. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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14.1%; Score 268.4; DB 1;
Best Local Similarity 55.3%; Pred. No. 1.5e-55;
Matches 543; Conservative 0; Mismatches 436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
COSTION: 49.1188
OTHER INFORMATION: /codon_start= 49
                                          1176 rrcrrcccrragaagag 1197
1298 TIGCTCACCCTAAAACTAAGCG 1319
                                                                                                                                                                Sequence 12, Application US/08662318
Patent No. 5827672
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: 36,637
TELECOMMUNICATION INFORMATION:
TELEPAX: 617720-3500
TELEPAX: 617720-3500
TELEPAX: 617720-2441
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
LENGTH: 1316 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
HYPOTHERICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: mat_peptide
LOCATION: 49..1185
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216 GACTITICCATTTCAACACGGTTGAAGAGGTTCATTCAAGATTCCAGAGTCTGAATGCTGA 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 TACCAGGATGGTCCTGGTGAATGCTGTCTACTTCAAAGGAAAGTGGAAAACTCCATTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.3%; Pred. No. 1.5e-55;
Matches 543; Conservative 0; Mismatches 436; Indels 3;
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12509
FILING DATE: herewith
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/315,831
ATTORNEY/AGENT INFORMATION:
NAME: PLUMEY: Bliabbeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET UNBER: 26,637
REFERENCE/TOCKET UNBER: 26,637
REFERENCE/TOCKET UNBER: C0279/7016
TELEPHONE: 617-720-3500
TELEPHONE: 617-720-3500
TELEPAX: 617-720-3500
TELEPAX: 617-720-3500
SEQUENCE CHARACTERISTICS:
LENGTH: 1316 base pairs

"VOR: NUMBER: Caid
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; LOCATION: 49..1185
PCT-US95-12509-12
        ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
CRIGINAL SOURCE:
ORGANISM: Homo sapi
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LOCATION: 49..1188
OTHER INFORMATION:
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336 AACTTACAATTTCCTGAGTTCTTGGTTTCGACTCAGAAAACATATGGTGCTGACT 395
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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Human Monocyte Blastase Inhibitor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: #600 Atlantic Ave.
STREET: #600 Atlantic Ave.
STREET: #80500
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1430;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.3%; Pred. No. 1.6e-55;
Matches 543; Conservative 0; Mismatches 436; Indels
                     TELEPHONE: (650) 855-0555;
TELEPHONE: (650) 855-0555;
TELEPHONE: (650) 855-0555;
TELEPHONE: (650) 855-010;
SEQUENCE CHARACTERISTICS:
LENGTH: 1430 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: EOSIHETO2
US-09-016-434-710
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                              TGCCGATGTCCACTGGCTTGGAGCTGGAAAGTGAAATAACCTATGACAAACTCAA
   AATGATGTATCAGAAGAAAATTTGCATATGGCTACATCGAGGACCTTAAGTGCCGTGT
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Parent No. 650038

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCES: 1490
CORRESPONDENCES:
STREET: 3174 FORTER DRIVE
CITY: PALLO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILLING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGCICACCCTAAAACTAAGCG 1319
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SULT 15
-09-016-434-710
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Search completed: March 11, 2004, 14:41:44
Tob time : 93.1303 secs

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CAATGGAGGATCTTTGTGTGGCAAACACACTCTTTGCCCTCAATTTATTCAAGCATCTGG 120
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ORGANISM: Homo sapiens
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Sequence 261, App
Sequence 126, Appl
Sequence 252, Appl
Sequence 178, Appl
Sequence 178, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 13440, A
Sequence 13440, A
Sequence 12440, A
Sequence 12440, A
Sequence 22703, Sequence 22703, Sequence 22703, Sequence 2740, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Appl
Sequence 17, Appl
                                                                                            March 11, 2004, 03:37:21 ; Search time 444.601 Seconds (without alignments) 15799.545 Million cell updates/sec
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1908
1 gaggagcattgcccgtcaga......aacaaaaaataaaaaagg 1908
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1: / cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*
2: / cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: / cgn2 6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
4: / cgn2 6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
5: / cgn2 6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
6: / cgn2 6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: / cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
7: / cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
8: / cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
10: / cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
11: / cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
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ALIGNMENTS

DB 14; Length 1908; NAME/KEY: misc feature ; OTHER INFORMATION: Incyte ID No. US20030119009A1 063646CB1 US-10-084-817-27 US-10-094-0-17-2/

Sequence 27, Application US/10084817

Publication No. US20030119009A1

GENERAL INFORMATION:
APPLICANT: Susan Stuart
APPLICANT: Staron E. Plon
APPLICANT: Jacon M. Shohet
ITILE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT FILING DATE: 2002-02-25
PRIOR PPLICATION NUMBER: 60/270,784
PRIOR PPLICATION NUMBER: 60/270,784

PRIOR FILING DATE: 2002-02-23
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                                                                                                                                DB 14;
                                                                                                                             Query Match
99.4%; Score 1896; D
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1899; Conservative 0; Mismatches
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 261
LENGTH: 1935
TYPE: DNA
ORGANISM: Home sapiens
US-10-106-698-261
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1151 TGGATGTGAATGAGGAGGGCACTGAAGCAGCCGCTGGCACAGGAGGTGTTATGACAGGGA 1210
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                                                                                                                                               GAGATGTTAGCATGTTGCTTCCAGATGAAATTGCCGATGTGCCACTGGCTTGG 900
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                                       671 AIGCTGICTACTICAAAGGAAAGTGGAAAACTCCATTIGAGAAGAAGTAAATGGGCTTT
                                                                                      721 ATCCTTTCGGTGTAAACTCGGCTCAGCGCACACCTGTACAGATGTGTACTTGCGTGAAA
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GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Wetzel, Uwe
APPLICANT: Wockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFRENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT APPLICATION NUMBER: DCT/US01/09847
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PATENTING VET. 2.1
SEQ ID NO 1566
LENGTH: 1900
TUPE: NUM
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OTHER INFORMATION: Genbank Accession No. US20040033502A1 Y00630
IS-10-240-425-1566
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98.1%; Score 1872.6; DB 12; Lengtl
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches 4; Indels
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Sequence 252, Application US/09962832
| Sequence 252, Application US/09962832
| Patent No. US20020110821A1
| SERREAL INFORMATION:
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1442 ACTAAATAAAAACACAGAAATAATTAGACAATTGTCTATTATAACATGACAACCTATTA
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Best Local Similarity 99.3%; Pred. No. 1.6e-213;
Matches 989; Conservative 0; Mismatches 7;
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Sequence 45, Application No. US20040043389A1

GENERAL INVEMATION.

GENERAL INVEMATION.

GENERAL INVEMATION.

TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels and the Diseases

TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels and the CURRENT PAPPLICANTION.

TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels and the Diseases

TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels and the Diseases

TITLE OF INVENTION: Risk Factors 40

CURRENT PAPPLICATION NUMBER: US/10/235,192A

NUMBER OF SEQ ID NOS: 49

SOFUTANTAL FALLS FACTOR FACTOR Windows Version 4.0

SEQ ID NO 45

IENGTH: 191395

TENGTH: 191395

CORANISM: Home sapiens

US-10-235-192A-45
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164654 GCCAAAAATTTAGAGAIGTTTTCTACATATTTCTGCTCTTCTGAACAACTTCTGCTACCTCCTCC 164595
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Best Local Similarity 99.3%; Pred. No. 1.8e-212;
Matches 990; Conservative 0; Mismatches 7; Indels 0; G
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                                                                                 Query Match 29.4%; Score 560; DB 9; Length 566; Best Local Similarity 100.0%; Pred. No. 4.1e-117; Matches 560; Conservative 0; Mismatches 0; Indels
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CORGANISM: Homo sapien
US-09-997-279-178
                        Homo sapien
; TYPE: DNA
; ORGANISM: HOMC
US-09-813-358-178
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Patent No. US20020048759A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
TITLE OF INVENITION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENITION: COMPOSITIONS OF OVARIAN AND ENDOMETRIAL CANCER
FILER REFERENCE: 210121.501
CURRENT APPLICATION NUMBER: US/09/813,358
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 222
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 178
LENGTH: 566
                                                                   GGATGTGAATGAGGAGGGCACTGAAGCAGCCGCTGGCACAGGGAGGTGTTATGACAGGGAG
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US-09-997-279-178/C
| Sequence 178, Application US/09997279
| Sequence 178, Application US/09997279
| Publication No. US20030059781A1
| GENERAL INFORMATION: USA
| APPLICANT: Chenault, Ruth A. APPLICANT: Chenault, Ruth A. APPLICANT: Xu. Jiangchun
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN AND ENDOMETRIAL CANCER FILE REFERENCE: 210121.501C1
| CURRENT APPLICATION NUMBER: US/09/997,279
| CURRENT FILING DATE: 2001-11-28
| NUMBER OF SEQ ID NOS: 230
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 178
| LENGTH: 566
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29.4%; Score 560; DB 10; Length 5
Best Local Similarity 100.0%; Pred. No. 4.1e-117;
Matches 560; Conservative 0; Mismatches 0; Indels
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                                               AGCCCCACCAGAACCTCTTCTCTCCCCATGGAGCATCTCGTCCACCATGGCCATGGTC
                                                                                                   TACATGGGCTCCAGGGCCAGCACCGAAGACCAGATGGCCAAGGTGCTTCAGTTTAATGAA
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Publication No. US20030059781A1
Publication No. US20030059781A1
Publication No. US20030059781A1
APPLICANT: Ku. Jiangchun
APPLICANT: Xu. Jiangchun
APPLICANT: Xu. Jiangchun
APPLICANT: Xu. Jiangchun
APPLICANT: Xu. Jiangchun
APPLICANT: Xu. Jiangchun
APPLICANT: Xu. Jiangchun
APPLICANT: Xu. Jiangchun
APPLICANTON: ComPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF OVARIAN AND ENDOMETRIAL CANCER
FILE REFERENCE: 210121.501C1
CURRENT PAPLICATION NOMBER: US/09/997,279
CURRENT PILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 230
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ for Windows Version 4.0
SEQ ID NO 66
IBNGTH: 503
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26.1%; Score 498.8; DB 10;
Best Local Similarity 99.6%; Pred. No. 3.2e-103;
Matches 500; Conservative 0; Mismatches 2;
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US-09-997-279-66
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| Patent No. US20020048759A1
| Patent No. US20020048759A1
| Patent No. US20020048759A1
| APPLICANT: Xu, Jiangchun
| APPLICANT: Pyle, Ruth
| APPLICANT: Stolk, John A.
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: COMPOSITIONS AND ENDOMBTRIAL CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN AND ENDOMBTRIAL CANCER |
| FILE REPERENCE: 210121.501 |
| CURRENT APPLICATION NUMBER: US/09/813,358 |
| CURRENT FILING DATE: 2001-03-21 |
| SOFTWARE: FastSRQ for Windows Version 4.0 |
| TYPE: DATE |
| TYPE: DATE |
| TYPE: DATE |
| ORGANISM: Home sapien |
| US-09-813-358-66
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Pred. No. 3.2e-103;
0; Mismatches 2; Indels 0
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Best Local Similarity 99.6%;
Matches 500; Conservative
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Sequence 13440, Application US/10029386
| Sequence 13440, Application US/10029386
| Publication No. US20030194704A1
| GENERAL INFORMATION: US20030194704A1
| GENERAL INFORMATION: David R. PAPPLICANT: Penn. Sharron G. APPLICANT: Hanzel, David R. APPLICANT: Hanzel, David R. TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (FILE REPRENCE: AEOMICA-X-2 (CURRENT PELICATION NUMBER: US/10/029,386 (CURRENT PELICATION NUMBER: 2001-112-20 (CURRENT PILING DATE: 2001-12-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13-20 (CURRENT PILING DATE: 2001-13
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                                                                                                                                                                                                                                                                                                             9; Length 482;
ORGANISM: Homo sapiens
FEATURE:
CTHER INFORMATION: MAP TO ACCOOSED.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.92
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.9
CTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
US-09-864-761-13940
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OTHER INFORMATION: MAP TO CHRIB.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.32
OTHER INFORMATION: WI HIT: M31551.1, SVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: P05120, EVALUE 1.00e-56
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24.9%; Score 475.6; DB 9
Best Local Similarity 99.2%; Pred. No. 5.9e-98;
Matches 478; Conservative 0; Mismatches 4
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PRICE NO. 129202004975A1

PRICE NO. 129202004975A1

APPLICANT: Name, Sharton G.

APPLICANT: Name, Sharton G.

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APPLICANT: Name, Sharton G.

APPLICANT: Name, Sharton G.

TITLE OF INVENTION: NAME: US/99/664,761

CURRENT APPLICATION NUMBER: US/99/664,761

PRIOR PELING DATE: 2010-02-04

PRIOR APPLICATION NUMBER: US/99/664,761

PRIOR APPLICATION NUMBER: US/99/664,761

PRIOR APPLICATION NUMBER: US/99/664,761

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PRIOR APPLICATION NUMBER: US/99/69/694

PRIOR APPLICATION NUMBER: US/99/694

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PRIOR APPLICATION NUMBER: US/99/694

PRIOR APP
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                                                                                                              302 CAGCAGATCCAGAAGGGTAGTTATCCTGATGCGATTTTTGCAGGCACACAGCTGCAGATAAA
                                                                                                                                                                                          369 ATCCATTCATCTTCGGCTCTCAGCTCTGCAATCAATGCATCCACAGGGAATTATTTA
                                      CAGCAGATCCAGAAGGGTAGTTATCCTGATGCGAT
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RESULT 14
US-10-029-386-27140
US-10-029-386-27140
Sequence 27140, Application US/10029386
Sequence 27140, Application US/10029386
Sequence 27140
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                                                                                                                                         295 GGCTGAAGATGAAGTTGAGGTATACATACCCCAGTTCAAATTAGAAGAGCATTATGAACT
                           355 GCAGCTGGAAAGTGAAATAACCTATGACAAACTCAACAAGTGGACCAGCAAAGAAAAT
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18.0%; Score 343.2; DB 14; Length 354;
Best Local Similarity 99.1%; Pred. No. 6.3e-68;
Matches 345; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA

OGGANISM: Homo sapiens

CTHER INFORMATION: EXPESSED IN LUNG, SIGNAL = 0.32

OTHER INFORMATION: EXPESSED IN LUNG, SIGNAL = 0.32

OTHER INFORMATION: EST HUMAN HIT: BF66685.1, EVALUE 0.00e+00

OTHER INFORMATION: NT HIT: M24657.1, EVALUE 0.00e+00

CTHER INFORMATION: SWISSPROT HIT: P05120, EVALUE 3.00e-47
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US-10-27-632-122703/C
US-10-27-632-122703/Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 108827.129
CURRENT PELIGATION NUMBER: US/10/027,632
CURRENT PELIGATION NUMBER: US/006

PRIOR PAPLICATION NUMBER: US 60/18,066

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1299-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

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Pred. No. 3.4e-69;
0; Mismatches 3; Indels 0;
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                                                                               Query Match 20.3%; Score 387.6; DB 14; Length 596; Best Local Similarity 99.0%; Pred. No. 6.8e-78; Matches 390; Conservative 0; Mismatches 40; Indels 0;
; OTHER INFORMATION: EST_HUMAN HIT: BF666685.1, EVALUE 0.00e+00
US-10-029-386-13440
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Best Local Similarity 99.2%;
Matches 352; Conservative 0
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Sequence 865, Application US/10029386

Sequence 865, Application No. US20030194704A1

Shellicant: Nemation No. US20030194704A1

APPLICANT: Penn, Sharron G.

APPLICANT: Rearch, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: REPRESSION ANALYSIS TWO

FILE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

CURRENT FAPLICATION WUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARER: Annomax Sequence Listing Engine vers: 1:1

SEQ ID NO 865

LENGTH: 544
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247 GGATGTGAATGAGGAGGGCACTGAGCAGCCGCTGGCACAGGAGGTGTTATGACAGGAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGATGTGAATGAGGAGGGCACTGAAGCAGCGCTGGCACAGGAGGTGTTATGACAGGGAG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 GGCTGAAGATGAAGTTGAGGTATACATACCCCAGTTCAAATTAGAAGAGCATTATGAACT
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                                                         1202 AACTGGACATGGAGGCCCACAGTTTGTGGCAGATCATCCGTTTCTTTT 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MAP TO ACO09802.13
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.33
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.33
OTHER INFORMATION: NT HIT: M31551.1, EVALUE 0.000+00
OTHER INFORMATION: EST HUMAN HIT: BF666685.1, EVALUE 0.000+00
US-10-029-386-865
                                                                                                              307 AACTGGACATGGAGGCCCACAGTTTGTGGCCAGATCATCCTTTTCTTTT 354
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GenCore version Copyright (c) 1993 - 2004	elc search, using sw model arch 10, 2004, 09:18:38; Sea: (wi S-10-084-817-27	able: IDENTITY NUC Gapox 1.0 Gapop 10.0, Gapext 1.0 27513289 seqs, 14931090276 res	Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	F⊣		16: em estom: * 17: em ges hum: * 19: em ges hum: * 20: em ges hum: * 21: em ges fun: * 22: em ges fun: * 23: em ges fun: * 23: em ges man: * 25: em ges pro: * 26: em ges pro: * 27: em ges pro: * 28: gb ges vr: *	red. No. is the number of score greater than or equal and is derived by analysis \$\\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\	1145 9 1126 9

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	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and orde them based on alignment. Location/Qualifiers 11248 /mol_type="genomic DNa" /mol_type="genomic DNa" /locate="SERPINB2" /gene="SERPINB2" /locus_tag="HCM5849"	Score 1241.6; DB 29; Length 1248; Pred. No. 1.7e-221; Mismatches 4; Indels 0; Gaps SCAAACACACTTTTGCCTCAATTTATTCAAGCATCTGGCA 12 SCAAACACACTTTGCCCTCAATTTATTCAAGCATCTGGCA 60		AATGAAGTGGGGAATGCAGTTACCCCATGACTCCAGAGAACTTTACCAGCTGTGGG TTCATGCAGCAGCAGTAACGCATGACTCCAGAGAACTTTACCAGCTGTGGG TTCATGCAGCAGCAGCAGAGGGTAGTTATCCTGATGCGATTTTGCAGGCACAAGCTGCA TTCATGCAGCAGAACGCAAGGTAGTTATCCTGATGCGATTTTGCAGGCACAAGCTGCA	GATAAATCCATTCATCCTTCCGCTCTCTGGCATCGAATGATGCTCCACAGGGAAT [TGTGCAGAAGGTTAGAAAAAGATTAATTCCTGGGTCAAGACTCAAAGGCAAA ATCCCAAACTTGTTACCTGAAGGTTCTGTAGATGGGGATACCAGGATGGTCCTGGTGAAT	GCTGTCTACTTCAAAGGAAAGTGGAAAACTCCATTTGAGAAGAAACTAAATGGGCTTTAT 72 GCTGTCTACTTCAAGGAAACTGGAACTCCATTTGAGAGAAACTAAATGGGCTTTAT 66 GCTGTCTACTTCGAGAAACTCGGAAACTCGATTGAGAGAAGAAGAAGAACTTGGGAAAAA 78 CCTTTCCGTGAAAACTGGCTGAACAGACTGAAAAA 78	CTAAACATTGGATACATAGAAGACCTAAAGGCTCAGATTCTAGAACTCCCATATGCTGGA [

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ALSSO163 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA Clone CSOD1040YG06 5-PRIME, MRNA sequence.
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized.
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53.9%; Score 1027.8; DB 9; Length 1126;
Best Local Similarity 98.1%; Pred. No. 1.3e-181;
Matches 1056; Conservative 13; Mismatches 5; Indels 3;
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AL574114 EST 31295449
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Homo sapiens
Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases I to 1126)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-ingth cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12934006.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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primer. Five prime end enriched, double-strand cDNA was
primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector, Library was normalized. For Contact GAAATTGCCGATGTCCACTGGCTTGGAGCTGCTGGAAAGTGAAATAACCTATGACAAA 993 GAAATIGCCGATGTGCCACTGGCTTGGAGCTGCAAAGTGAATAACCTATGACAAA GCTCAGATTCTAGAACTCCCATATGCTGGAGATGTTAGCATGTTCTTGTTGCTTCCAGAT 1053 GCTCAGATTCTAGAACTCCCATATGCTGGAGATGTWAGCATGTTCTTGTTGCTCCCAGAT 753 CCTGTACAGATGATGTACTTGCGTGAAAAGCTAAACATTGGATACATAGAAGACCTAAAG Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9202.f F
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi-seq-CSOD1040BD03NP1&cluster=9202.f. Contac
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOD1040BD03NP1. Gaps . М

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Analysis of the mouse transcriptome based on functional annotation Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

B Nature 420, 563-573 (2002)

E (bases ito.1965)

Adachi, ., Alzawa, K., Akimura, T., Hara, A., Hashizume, W.,

B Hayashida, K., Hayatsu, M., Hiranco, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Katoh, H., Kawai, J., Kohina, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Ohsato, N.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Sano, H., Sasai, C., Saltoh, H., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Sahibata, K., Shiraki, T., Takaku-Akahira, S.,

Takeda, Y., Tagawa, A., Takahsshi, P., Takaku-Akahira, S.,

Takeda, Y., Tagami, M., Tagawa, A., Takahsshi, P., Takaku-Akahira, S.,

Nuramatsu, M., and Hayashizaki, Y. Tayari, T., Tagami, M., Towari, Y., Yasunishi, A.,

Direct Submission

Sogabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Nuramatsu, M., and Hayashizaki, Y. Takaku-Akahira, S.,

Rakeda, Y., Tanashizaki, Y., Saltoh, Y., Toya, T., Yasunishi, A.,

Nuramatsu, M., and Hayashizaki, Y. Takaku-Akahira, S.,

Takeda, Y., Tanashizaki, Y., Japani, J., Toya, T., Yasunishi, A.,

Nuramatsu, M., and Hayashizaki, Y. Takaku-Akahira, S.,

Takeda, Y., Tanasan, A., Tayan, Y., Yasunishi, A.,

Nuramatsu, M., and Hayashizaki, Yasunishi, A.,

Nuramatsu, M., and Hayashizaki, Y.

Direct Submission

Sogabe, Y., Tanasan, A., Yasunishi, A., Yokohama, A.,

Submitted (16-APP-2002) Yoshihide Hayashizaki, The Institute of Genome Grounic Sciences Center and Genome Excenter Contributed to Division of Experimental Animal Research in Nouse Genome

Broder, J. Japan (18-APP-2002) Yoshimal Research in Riken Contributed to Division of Experimental Animal Research in Riken Contributed to Division of Experimental Animal Research in Rike
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and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGAGAACAACCAGATTGAAACAATGGAGGATCTTTGTGTGGCAAACACACTCTTTGCCC
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Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl10020L09 product:serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2, full insert sequence. AKO81487

AKO81487. G1:25349182

MITC: CAP trapper.

Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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   TCTGCTCTTCTGAACMACYTCYGCTACCCACTAAATAAAAACACAGAAATAATTAGACAA
                                                                                            394 ITGECENTALABACATGACAACCCEATTAATCATTTGGTCKECTAAAAAGGGRECATGCC
                                                                                                                                                                          CATTTAGATTTTCCTTACTATCAGTTTATTTTTATAACATTAACTTTTACTTATTT
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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High-efficiency full-length cDNA cloning
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Best Local Similarity 73.0%; Pred. No. 1.2e-176;
Matches 1366; Conservative 0; Mismatches 477; Indels
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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    1952
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79 70 139

130 199 190 259 250 319

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On Feb 16, 2001 this sequence version replaced gi:12944080.
Contact: Genoscope
Genoscope - Centre National Ge Sequencage
BP 191 91006 ENRY cedex - France
Email: seqref@genoscope.ons.fr, Web: www.genoscope.ons.fr
was not nomalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9202.f For more information about this cluster, see
http://ww.genoscope.ons.fr/
cgi-bin/cluster.cgi?seq=CSODH002CE03NPl&cluster=9202.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODH002CE03NPl.
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LINE) Homo sapiens cDNA
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/note="Pector: pCMVSPORT_6, lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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llarity 88.7%; Pred. No. 6.3e-171;
Conservative 77; Mismatches 46; Indels 3;
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                                 1046 CATGGAGGACGCCTTCAACAAGGGACGGCCAATTTCTCAGGGATGTCGGAGGAATGA
                                                                 814 CATGGAGGACGCCTTCAACAAGGGACGGGCCAATTTCTCAGGGATGTCGGAGGGAATGA
                                                                                                   1106 CCTGTTTCTTTCTGAAGTGTTCCACCAAGCCATGGTGGATGTGAATGAGGAGGGCACTGA
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ORIGIN

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ALSS2817
ALSS2817
ALSS2817 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODIO68YK02 3-PRIME, mRNA sequence.
ALSS2817.2 GI:31274632
RESULT 8
ALSS2817/C
LOCUS
DEFINITION
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Homo sapiens (human) Homo sapiens ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primatee, Catarrhini, Hominidae, Homo. 1 (1091) (REFERENCE AUTHORS

Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12892068.
Contact: Genoscope
Contact: Genoscope
BP 191 91006 EVAY codex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9202.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CSDDI068BF01NP1&cluster=9202.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllangth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI068BF01NP1.) Coganism="Homo sapiens"

/mol Lype="mRNA" \
/db xref="taxon:9606"
/clone="CSODIOGSYKO2"
/tissue type="HACCENTA COT 25-NORMALIZED"
/clone=lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized. TITLE JOURNAL COMMENT FEATURES

TGAAATTGCCGATGTCCACTGGCTTGGAGCTGCTGGAAAGTGAAATAACCTATGACAA 990 TGAAATTGCCGATGTGCCACTGGCTTGGAGCTGCTGGAAAGTGAAATAACCTATGACAA Gaps Length 990; 49.7%; Score 947.6; DB 9; 96.7%; Pred. No. 1.2e-166; tive 18; Mismatches 14; Query Match Best Local Similarity 96.74 Matches 957; Conservative 872

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1050 1110 1170 1230 9 871 811 691 631 751 CCGCTGGCACAGGAGGTGTTATGACAGGGAGAACTGGACATGGAGGCCCACAGTTTGTGG ACTICAACAAGTGGACCAGCAAAGAC-AAAATGGCTGAAGATGAAGTTGAGGTATACATAC CCCAGITCAAAITAGAAGAGCATTAIGAACTCAGATCCATTCTGAAAAGCATGGGCATGG cccagircaaariaaaagaagcarrargaacrcagarccarrcrgagaagcarggaargg <u> AGGACGCCTTCAACAAGGACGGGCCAATTTCTCAGGGATGTCGGAGAGAAATGACCTGT</u> AGGACGCCTTCAACAAGGGACGGCCAATTTCTCAGGGATGTCGGAGAGGAATGACCTGT 1111 ITCTTTCTGAAGTGTTCCACCAAGCCATGGTGGATGAGGAGGAGGGCACTGAAGCAG 750 Trentreraagreneeaceaceaaceareereaareraareagaggaggaeereaag 932 870 1051 1171 930 991 810 g 임 셤 ò ď ઠે 셤 ઠે à ò

1290 1350 1410 571 451 GCAGATTTTGCTCACCCTAAAACTAAGCGTGCTGCTTCTGCAAAAGATTTTTGTAGATGA GCTGTGTGCCTCAGAATTGCTATTTCAAATTGCCAAAAATTTAGAGATGTTTTCTACATA 1231 CAGATCATCCGTTTCTTTTTTTTTTTATGCATAAGATAACCAAGTGCATTTTATTTTTCG 570 GCAGATITICCICACCCIAAAACTAAGCGIGCIGCTICTGCAAAAGATTTTTGTAGATGA 510 GCTGTGTGCCTCAGAATTGCTATTTCAAATTGCCAAAAATTTAGAGATGTTTCTACATA 630 1351 1291 g ð ठ P δ g

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T. (bases 1 to 1044)

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Euli-length cDNA libraries and normalization

M. Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:12892133.

Contact: Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

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BF 191 910 SONTY cedex - France

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1041)

1 (bases 1 to 1041)

2 Li,Wa.B., Gruber,C., Jessee,J. and Polayes,D.

S. Full-length cDNA libraries and normalization

Unpublished (2001)

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Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 9202.f For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CsOD1013BH11QP1&cluster=9202.f. Contact :

Feng Liang Email: fliang@lifetech.com URL:

http://fullength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSOD1013BH11QP1.
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| And _ Lyppe="mRNA" |
| Ab _ Xref="tax01:9606" |
| Clone="CS01013Y022" |
| Cissue _ Lype="PLACENTA COT 25-NORMALIZED" |
| Clone _ Ilb= "Homo sapiens PLACENTA COT 25-NORMALIZED" |
| Anote="lst strand cDNA was primed with a NotI-oligo(dT) |
| Anote="lst strand cDNA was primed with a NotI-oligo(dT) |
| Anote="lst strand cDNA was primed with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AGCATTGCCCGTCAGACAGCAACTCAGAGAATAACCAGAGAACAACCAGATTGAAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCAAGCCCCACCCAGAAACCTCTTCCTCTCCCCATGGAGCATCTCGTCCACCATGGCCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGGATCTTTGTGTGGCAAACACACTCTTTGCCCTCAATTTATTCAAGCATCTGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 gdadgarcrindrgigigicaaacacrintrgcccricaartratrcaagcarcriggcaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCAAGCCCCACCCAGAACCTCTTCCTCCCCATGGAGCATCTCGTCCACCATGGCCAT
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llarity 91.1%; Pred. No. 3.3e-160;
Conservative 68; Mismatches 18; Indels 1.
                                                                                                              1000
                                                                      900 GAGCTGCTGGAAAGTGAAATAACCTATGACAAACTCAAC
                                                                                               GAGCTGCAAAAGTGAAATAACCTATGACAAACTCAAC
                                                                                                                                                                                                                                                                                                                                                           sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                      sapiens
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Best Local Si
Matches 894
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                RESULT 12
BX396200
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       /organism="Homo sapiens"
/mol type="manya"
/db xref="taxon:5606"
/clone="CSODIO78YH02"
/clone="CSODIO78YH02"
/clone lib="PlaceEnrya COT 25-NORMALIZED"
/clone lib="Homo sapiens PlaceTry COT 25-NORMALIZED"
/note="Ist strand cDNa was primed with a NotI-oligo (dT)
/note="lst strand cDNa was primed with a NotI-oligo (dT)
/note="lst strand cDNa was primed with a NotI-oligo (dT)
/note="lst strand cDNa was primed with Not I and cloned into the Not I and EORN was sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAATGGAGGATCTITGIGIGGCAAACACACICITTGCCCTCAATTAITCAAGCATCTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAAAAGCAAGCCCCACCCAGAACCTCTTCCTCCCCATGGAGCATCTCGTCCACCATGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAAGCAAGCCCACCAGAACCTCTTCCTCTCCCCATGGAGCATCTCGTCCACGTGG
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                                                                                                                                                                                                                                                                                                                                                                GAGGAGCATTGCCCGTCAGACAGCAACTCAGAGAATAACCAGAGAACAACCAGATTGAAA
                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                        Score 925.4; DB 9; Length 1000;
Pred. No. 1.6e-162;
0; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.8%;
Matches 937; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602
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/organism="Homo sapiens"
//organism="Homo sapiens"
//organism="Mon"
//ob xref="taxon.9606"
/clone="CSODH002VJ05"
/clone="CSODH002VJ05"
/clone lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/clone lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/note="Voctor: pCMVSpORT 6; lst strand cDNA was primed with a NotI-ollgo(dT) primer. Five prime end enriched with a NotI-ollgo(dT) primer. Five prime end enriched double-strand cDNA was digested with Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 ATGGAGGATCTTTGTGTGGCAAACACACTCTTTGCCCTCAATTTATTCAAGCATCTGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGCATTGCCCGTCAGACAGCAACTCAGAGAATAACCAGAGAACAACCAGATTGAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TICATGCAGCAGATCCAGAAGGGTAGTTATCCTGATGCGATTTTGCAGGCACAGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATATTCGACTCTGTCAGAAATATTACTCCTCAGAACCCCCAGGCAGTAGACTTCCTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATATTCGACTCTGTCAGAAATATTACTCCTCAGAACCCCAGGCAGTAGACTTCCTAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTGCAGAAGAAGCTAGAAAAAAATTAATTCCTGGGTCAAGACTCAAACCAAAGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCCAAACTTGTTACCTGAAGGTTCTGTAGATGGGGATACCAGGATGGTCCTGGTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arcccaaacrigriaccigaaggricigiagargaggaraccaggarggricigagar
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9202.f For more information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi-pseq=CSDH002CE03QPl&cluster=9202.f. Contac Feng Liang Email : fliang@lifetech.com URL : http://full.ength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODH002CE03QPl.
Location/Qualifiers
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Homo sapiens (human)

Homo sapiens

ENARAYOLA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ENARAYOLA; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1201)

S Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length CDNA libraries and normalization

L Unpublished (2001)

On Reb 15, 2001 this sequence version replaced gi:12900443.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Genoscope - Genoscope cns. Fr www.genoscope.cns.fr

was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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ALSS7133 Homo sapiens T CELLS (JUXXAT CELL LINE) Homo sapiens CDNA
Clone CSODH002YJOS 5-PRIME, mRNA sequence.
ALSS7133
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AL545835 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI023Y006 5-PRIME, mRNA sequence.
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1 (Dases 1 to 989)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization

Unpublished (2001)
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                                                                                               CTAAACATTGGATACATAGAAGACCTAAAAGGCTCAGATTYTAGAACTCCCATATGCTGGA 887
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primer: Five prime end enriched, doubbe-sstrand cDNA was
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                                                                                                                                                                                                      CTGCTGGAAAGTGAAATAACCTATGACAAACTCAACAAGTGGAC 946
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http://www.genoscope.cns.fr/
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Feng Liang Bmail : fliang@alifetech.com URL :
Feng Liang Bmail : fliang@alifetech.com (InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSOD1023BH03QPl.

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SUMMARIES

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/db_xref="taxon:9606"
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	AAGGGCAGCAGAAGGAAGGACCAGGGCAAAGGAAGGAAG	1411 AAAAGGGGAAAAAGGTAGAACAGAAAGGGAAATGGGTAAATGAAAAGAAAG	AGATGAAAAGAGATTAAAAAGAACAAAAACCCAAAGAAAG	1957 ACATACTGAGAATACTTTCAGCGGCCCTGGAGGGGCCAGCGTGGACACCAAGGAGGC 2016	GGAGACCGAGAGCGAGAGCTCAAACGAGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	CAGGARGCAGGAGCCGATCGAAAACTCAGAGAAGGAAGGAAGGAGGAGGAGGAGGAGGAGGAGGAG	2317 AGATGGCTTGTCAGATGACAATACCATTCAGTGTTTCACTCCTAAAGGTTCATCTCT 2376 2101 AGATGGCTTGTCAGATGACAAAACCATTCAAGTGTTTCACTCCTAAAGGTTCATCTCT 2160 2377 CAAGATAGAAGAGCGAGCAGAATTTTTGAATAAGTCTGTGCAGAAAAGGTTCATCTCT 2160 2377 CAAGATAGAAGAGCGAGCAGAATTTTTGAATAAGTCTGTGCAGAAAAGGTGTCAA 2436 2161 CAAGATAGAAGAGCGAGCAGAATTTTTGAATAAGTCTGTGCAGAAAAGCAGTGTCAA 2220 2437 ATCGACCCATCAAGCAGAATTTTTTGAATAGCAGCAGAAAAGCAGAAAAACCAGAAAAAGCAGAAAAAA

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                 TTTCCGACTTAGTCCTCGGGAAGAAGTTTCAGACTACAAGGTATCATGGAACATTTCAA
                                                     GCTGACCTGTCCAGACATCATCTGGTCTCCCTGAACCTGAAATCACACCATGGATGTTT
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Weintraub, L.A., Mohr-Tidwell, R.M., Peluso, D.C., Fulton, R.S. Leckte, M.P. and Green, E.D. A collection of 1814 human chromosome 7-specific STSs Genome Res. 7 (1), 59-64 (1997) 9718344 9037602 1 (Dases I to 3610) Green, E.D.
                                                                                          Human chromosome 7 STSs (1997)

Human chromosome 7 STSs (1997)

L Unpublished (1997)

Synonyms: CALD1

GDB: GDB: 3755080

GDB DSEG: CALD1

Confact: Eric D. Green

Gonome Technology Branch

National Human Genome Research Institute/NIH

49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD. 7el: 3014002201

Fax: 3014002201

Fax: 3014004735

Email: egreen@nhgri.nih.gov

Primer B: CTTTCTTTATAGGTCATC

STS size: 289

PCR Profile:
                                                                                                                                                                                                                                                                                                           0.00 minute(s)
0.17 minute(s)
1.00 minute(s)
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/ mol_type="genomic DNA"
/ db_xref="taxon:9606"
/ map="7"
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	1261 GATAAAGGAAGAAGAAAAGGGCAGCAGAGAAGAGGAGGATAAAAGAGAAAAAAAA	Db 1381 AGAGCAGAAACGTAACAAGCAAGAAAAAACGTGCCATGCAAGAAAAGAT 1440	1501 AGAAGATAAACTTCAGACAGCTGTCCTAAAGAAACAGGAGAGAGA	Db 1621 AGATGAAAAGATTAAAAAGGACAAAGAACCCAAAGAAGAAGTTAAGAGCTTCATGGATCG 1680 Oy 1897 AAAGAAGGAATTTACAGAAGTTAAGTCGCAGAATGAGAATTCATGACCCACAAACTTAA 1956 Db 1681 AAAGAAGGATTTACAGAAGTCGCAGAATGAGAATTCATGACCCACAAACTTAA 1740 Oy 1957 ACATACTGAGAATACTTTACGCCGCCTGGAGGCCAGGCGAGGCCACAAGGC 2016	DB	Db	Db 1981 GAGGAGGAAGCAGGAAAGCCGAACGACGAAACTTCAGAGAAGAAGAAGAAGAGCT 2040 Cy 2257 AAAGGAAGATTGAAAGCCGAAGAGCTGCTGAGAAACGCCAGAAGATGCCAGA 2316 Db 2041 AAAGGAAGAGTTGAAAAGGCGAAGAAGAGCTGCTGAGAAACGCCAGAAGATGCCAGA 2316	Oy 2317 AGATGGCTTGTCAGATGACAACAACCATTCAAGTGTTTCACTCCTAAAGGTTCATCTTCT 2376 Db 2101 AGATGGCTTGTCAGATGACAACCATTCAAGTGTTTCACTCCTAAAGGTTCATCTTCT 2160 C2377 CAAGATAGAAGAGCAGCAGAATTTTTGAATAAGTTGTGCAGAAAAGGTTCATCTCT 2160 Db 2161 CAAGATAGAAGAGCAGAATTTTTGAATAAGTTGTGCAGAAAAGGTGGTGTTCAA 2436 Db 2161 CAAGATAGAAGAGCAGAATTTTTGAATAAGTCTGTGCAGAAAAGCAGTGTGTCAA 2220 Oy 2437 ATCGACCCATCAAGCAGCAAATAGTCTGTGCAGAAAAGCAGTATACCAG 2496

Yammalia, Butheria, Primetes, Catarthiti, Honinidae, Hono. JUNESTER C. C., Mark and Keeman, M. Weils, A. Amid.C., Osanger.A., 11111		GCGGGGGCCCCCCCGGGTGGAAGCCGCAAAAGGCTGGAGGGGCTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT
Mammalia; Eutheria; Primates; Catarthin; Hominidae; Home. [Labse: 10, 4031] [Labse: 10, 4031] Disect Sim.M. and Memean, M. Weil, B., Amid, C., Osanger, A., The Osong, G., Sam.M. and Memean, S. Memean Date Care of Michaelsian Disect Simulasion Disect Simulasion Disect Simulasion Submitted (177A0G-203) MIPS, Ingolstaedter Lander: 1, D-85764 Newherberg, OSRAMT, Contact Confort; Display and Concorting and Care of Miles Care of	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	68686868686868686
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면본 원급단 본 표? 어떤 전기 (1) to:	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (CE 1 (bases 1 to 4091) RS Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Pobo,G.; Han,M., and Wiemann,S. (TM The German Human cDNA Consortium Direct Submissan Submitted (27-Aug-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherborg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKPZD); Email s.wiemann@dkfz.heidelberg.de; Clone from S. Wiemann, Molecular Genome Project Research Conter (DKPZD); Email s.wiemann@dkfz.heidelberg.de; sequenced by Qiagen (Hilden)Germany) within the cDNA sequencing consortium of the German Genome Project This clone (DKPZD686A06190) is available at the RZDD in Berlin. Please contact the RZDD: Reseourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/CDNA/. Location/Qualifers lu 4091 // Clone="DKFZp686A06190" // Clone="DKFZp686A06190" // Clone="DKFZp686A06190" // Clone="DKFZp686A06190" // Clone="DKFZp686A06190" // Clone="DKFZp686A06190" // Clone="DKFZp686A06190" // Clone="DKFZp686A06190" // Gev stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult" // Adv stage="adult"	60.0%; Score 2222.6; DB 9; Length 4091; Llarity 96.9%; Pred. No. 0; Conservative 0; Mismatches 19; Indels 56; Gaps AGAAAGACAACGAAAAGGAGGAAGAGGAAAGCGAAACCAAACGAGGGATH GABAAGAAACCAAAAAAAGGAGGAAGAGAAAACAAACAAA

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Hayashi, K., Hashida,T., Asada,K., Kotani,H., Kato,I. and Sobue,K..
DNA encoding a protein comprising calmodulin-and actin-binding human caldesmon peptide fragment
human caldesmon peptide fragment
Patent: US 5739008-A 14 14-APR-1998;
Location/Qualifiers
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*source: cell_type=Hela;
Key Location/Qualifiers
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/product='human ca
polyA_signal 2103. .2108
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Location/Qualifiers
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/organism="Homo sapiens"
/mol type="genomic RNA"
/db_xxef="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                  Query Match
42.4%; Score 1570.2;
Best Local Similarity 94.5%; Pred. No. 0;
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                                                                                                             GACTIGAGACCAGGAGACGIATCCAGCAAGCGAAACCTCTGGGAAAAGCAAICTGTGGAT
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28-MAR-1991 JP 91P 89106
HAYASHI KENICHIRO, HASHIDA HISASHI, ASADA KIYOZOU, PI
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| Hayashi,K., Hashida,T., Asada,K., Kotani,H., Kato,I. and Sobue,K.
| Proteins comprising calmodulin- and actin-binding human caldesmon polypeptide fragments
| Patent: US 5532337-A 14 02-JUL-1996; | Datent | Location/Qualifiers GAAAAGATTAAAAAGGACAAAGAACCCAAAGAAGAAGTTAAGAGCTTCATGGATCGAAAG GAAAAGATTAAAAAGGACAAAGAACCCAAAGAAGAAGTTAAGAGCTTCATGGATCGAAAG 1961 ACTGAGAATACTTTCAGCCGCCCTGGAGGGGCCCAGCGTGGACACACAAGGAGGCTGAG 882 edceccococcadereda Accedeca Anadocreda Accercor Corcerco Cocococo Associated Acces Associated Acces Acces Associated Acces Acces Acces Associated Acces GAGGAACTCAAGAAAAAGAGGAGGAGAGAAGGAAGGTCCTGGAGGAGGAAGAGCAGAAGAG 762 AAGGGATTTACAGAAGTTAAGTCGCAGAATGGAGAATTCATGACCCACAAACTTAAACAT GGCGCCCCCCAGGTGGAAGCCCGGCAAAAGGCTGGAGGAGCTTCGTCGTCGTCGCCGGGGAG GCTAAAAGAGAAAAGCTCCAAGAAGACAAGCCTACCTTCAAAAAAGAAGAGATCAAAGAT AGGAAGCAGGAAGCCGATCGAAAACTCAGAGAGGAAGAAAAAGAGAAGAGGAGGAGGTAAAAG 1062 AGGAAGCAGGAGGAAGCCGATCGAAAACTCAGAGAGGAGGAAGAAGAAAAAAGGAGGCTAAAG GATAAACTTCAGACAGCTGTCCTAAAGAAACAGGGAGAAGAGAAGGGGAACTAAAGTGCAA **AAGGGATTTACAGAAGTTAAGTCGCAGAATGGAGAATTCATGACCCACAAACTTAAACAT** GAAGAGATTGAAAGGCGAAGAAGCAGAAGCTGCTGAAAACGCCAGAAGATGCCAGAAGAT CAAGAAAGATACGAGATAGAGGAAACAGAAGTCACCAAAGTCCTACCAGAAGAATGAT 4; Gaps PAT Length 2215; 93; Indels . 9 DB DNA Score 1570.2; Pred. No. 0; 0; Mismatches 2215 bp US 5532337. .2215
 /organism="unknown"
 /mol_type="unassigned DNA" 123421 Sequence 14 from patent Query Match Best Local Similarity 94.5%; Matches 1660; Conservative GI:1603291 Unknown. Unclassified. 123421.1 2321 ò

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BC040354.1 GI:25955665
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                                                                                    1242 ATAGAAGAGCGAGCAGAATTTTTGAATAAGTCTGTGCAGAAAAGCAGTGGTGTCAAATCG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (bases 1 to 4130)

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Rlausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Schmutz, J., Myers, R.M.,

Generation and initial analysis of more than 15,000 full-length

Numan and mouse oDNA sequences

Nall, Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
4130 bp mENA linear PRI 07-OCT-2003
MGC:21352 IMAGE:4753285), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 28 Row: p Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15149468.
Location/Qualifiers
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowie, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Submission Submitted (27-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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/db_xref="taxon:9606"
/clone="MGC:21352 IMAGE:4753285"
/tissue_type="Skin, squamous cell carcinoma"
/lab_host="MHOE" Skn4"
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us-10-084-817-30.rge

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1205 CATGAAAAGATGGAAGAGGAAGACAAGGAAAGAGCTGAGGGCAGAGAGGGCAAAGGTTGGAA 1264
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GCTCTGGAGCGGCAGAAGGAGTTCGACCCAACAATAACAGATGCAAGTCTGTCGCTCCCA
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                                                                                                                             GAAAGTCGCCAAGAAAGATACGAGATAGAGAAACAGAAACAGTCACCAAGTCCTACCAG
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        1 (bases 1 to 2137)
Hayashi, K., Hashida,T., Asada,K., Kotani,H., Kato,I. and Sobue,K.
DNA encoding a protein comprising calmodulin-and actin-binding human caldesmon peptide fragment
human caldesmon peptide fragment
Patent: US 5739008-A 13 14-APR-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                      AAGAAGTTAAGAGCTTCATGGATCGAAAGAAGGGATTTACAGAAGTTAAGTCGCAGAATG
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                                                                                                                               Score 1481.6; DB 6; Length
Pred. No. 1.6e-306;
0; Mismatches 54; Indels
                                                                                     /organism≃"unknown"
/mol_type="unassigned DNA"
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Similarity 96.4%;
8; Conservative
Unclassified
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Hayashi,K., Hashida,T., Asada,K., Kotani,H., Kato,I. and Sobue,K.
Hayashi,K., Hashida,T., Asada,K., Kotani,H., Kato,I. and Sobue,K.
Proteins comprising calmodulin- and actin-binding human caldesmon polypeptide fragments
Patent: US 5532337-A 13 02-JUL-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCCAGTAAACCCATGTATATTATCACTATATTTAATAATCACAGTCTAGAGATGTTCAT
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/mol_type="unassigned
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Sequence 13 from patent
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123420.1 GI:1603290
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GTCAACAGAAGATCCAAGTTTAAAATTGCCTGCGGAATGTGTGCAGTATCTAGAAAAATG 3191
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Hayashi, K. and Sobue, K.
Direct Submission
Submitted (26-JUL-1991) Kenji Sobue, Osaka University, Medical
School, Biomedical Research Center, Department of Neurochemistry
and Neuropharmacology; Kita-ku, Osaka 530, Japan
(Tel:81-6-6445-6879, Fax:81-6-6445-6879)
                                                                                                                  CTC--TTTTGTATTTATGTTGATTTACTAAATTGGGGTTCATTATCTTTTTTTCATA
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GGAACCTCTGGGAAAAGCAATCTGTGGATAAGGTCACTTCCCCCACTAAGGTTTGAGACA
                                                                 GTTCCAGAAAGAACCCAAGCTCAAGACGCAGGACGAGGTCAGTTGTAGAGGGCTAATTCG
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                                          GTTCCAGAAAGAACCCCAAGCTCAAGACGCAGGACGAGCTCAGTTGTAGAGGGCTAATTCG
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Homo sapiens mRNA for l-caldesmon II, complete cds
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HeLa S3"
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Pred. No. 1.6e-306;
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AGCCGGCAGCCTCGGATCTTCCTGTTCCTGCAAGGTGTACGCAACATCAAGAGTATGT
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
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Matches 3140; Conservative 0; Mismatches 21; Indels 1;
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             28-SEP-2000; 2000US-0236034P.
28-SEP-2000; 2000US-02361109P.
29-SEP-2000; 2000US-023611019P.
29-SEP-2000; 2000US-0236891P.
02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237173P.
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Weaver Z;
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Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
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7-SEP-2000
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(AVAL-) AVALON PHARM.

Horrigan S; Endress G, Ebner R, Carter KC, Augustus M, Weaver Z; Young PE, i Soppet DR,

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 6941; 44pp; English

The present invention describes a method (M1) for screening for an anticomplastic agent. The method involves exposing cells to a chemical agent
to be tested for anti-neoplastic activity, determining a change in
expression of at least one gene (I) of a signature gene set, where (I)
comprises a sequence (S) selected from 8447 sequences (given in ABL61664
comprises a sequence (S) selected from 8447 sequences (given in ABL61664
comprises in indicative of anti-neoplastic activity. (I) has cytostatic
activity and can be used in gene therapy. M1 can be used for screening an
anti-neoplastic agent, and can be used for producing a product which is
anti-neoplastic agent. M1 can be used in the treatment of cancer such
to fm1, and the data is sufficient to convey the chemical structure and/or
properties of the agent. M1 can be used in the treatment of cancer such
as colon, breast, stomach, lung, thyroid, ossophageal, ovarian, kidney,
prostate or pancreatic cancer, adenocarcinoma, clear call
cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's

} }	C tumour	
g g	30 Sequence 3610 BP; 1322 A; 622 C; 96	3 G; 703 T; 0 U; 0 Other;
Ōďž	Query Match Best Local Similarity 99.3%; Pred. Matches 3140; Conservative 0; Mis	3116.4, DB 6, Length 3610; No. 0; matches 21; Indels 1; Gaps 1;
5 6	22 CIGCCIGCCGCCIGCTIGCTCTCTGGCTGTG	GGCTGTGCTCCTGCTTAAAGAAATCAGTCCTTCC 276
à	277 TTTCGACTTAGTCCT	CTACAAGGTATCATTGGAACAT
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e è	397	CCATGGATGATTT 45
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à i	517 AAT	CGCCTACCAGAGGAATGACGATGATGAAGAGGAGGAGGACGGGGGAACGGGGCGCGCGC
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ò	637	GTGTGCCTGAGGAGGAGGAGAAGACCACCAC 696
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ò	937 AACAGAAACAGTCACCAAGTCCTAC	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a cissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, of rung toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences
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                                                                                                                                                   Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
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Pred. No. 0;
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                                                                                                                               Gene #2407 used to diagnose liver cancer
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Best Local Similarity 99.3%;
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                                                      ABN95909 standard; DNA; 3610
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s; breast cancer monitoring;
t; breast cancer staging; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AABAAAAGTGCGGCGACAGTTATTCCTTT 3378
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04-OCT-2001; 2001US-00974298
                                05-OCT-2000; 2000US-0238331P
                                                                                                                                        WPI; 2003-182653/18.
                                                                   (CHEN/) CHEN
                                                                                                       Chen H;
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New cDNAs, which are differentially expressed in (metastatic) breast cancer useful for diagnosing or staging, breast cancer, or for monitoring the treatment of breast cancer in an individual.

Claim 1; SEQ ID NO 36; 30pp; English

The invention describes a combination of cDNAs (designated BC-CDNAs), which are differentially expressed in breast cancer. The combination includes 152 cDNA sequences, or their complements. The protein encoded by any of these BC-CDNAs is useful for screening several molecules or compounds to identify at least one ligand that specifically binds the protein, producing or preparing polyclonal or monoclonal antibodies, or burifying antibodies from a sample. The antibodies which specifically bind the protein differentially expressed in breast cancer is useful for detecting the expression of a protein in a sample. The BC-CDNAs are also useful for diagnosing, monitoring the treatment of, or staging, breast cancer associated CDNA. Note: The sequence data for this patent did not form a part of the printed specification, but was obtained in electronic format directly from the US patent office at segdata.uspto.gov/sequence.html?DocID=20020156263

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Sequence 4547 BP; 1496 A; 849 C; 1033 G; 1169 T; 0 U; 0 Other;

Gaps Length 4547; 9; Indels 766; Score 1793.6; DB 7; Pred. No. 0; 0; Mismatches 9; 1 Query Match Best Local Similarity 76.9%; Matches 2585; Conservative ઠે

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106	AAAGCCAGGAGGAACAGTGGTAATGTCATTAAAAAATGGGC 113
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92EP-00302591

Kato I, Kotani H, Ĥ Hashida 91JP-00358040 SOBU/) SOBUE K. TAKI) TAKARA SHUZO CO LTD. Asada K, 29-MAR-1991; 27-DEC-1991; Χ, Hayashi

Polypeptide(s) with calmodulin- and actin binding activities - useful for treating and diagnosing cancer and regulating digestive tract motility as vasodilators. WPI; 1992-325651/40

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Disclosure; Page 33-34; 47pp; English.

cons that encode polypeptide of human caldesmon were selected from a clones that encode polypeptide of human caldesmon were deduced by DAB sequence and the amino acid sequence encoding human caldesmon were deduced by DAB sequence analysis. Next, the inventors prepared polypeptides of various lengths, and looked for the functional domain of human caldesmon polypeptide, the functional domain of human caldesmon polypeptide. There are two forms of caldesmon. The form of higher mol. Wt. is called type I and the form of lower mol. Wt. is called type II. 312AA is a not polypeptide that is the C-terminal portion of types I and II. 122AA and called type I and that is the C-terminal portion of types I and II. 122AA and sequence of 312AA, and 94AA and 90AA are polypeptides that have a sequence of 118 AA that are in the central portion on the N-terminal continual portion of 118AA, there are residues Met-Ala that originated from a PCR primer, of 118AA, there are residues Met-Ala that originated from a PCR primer. Criginated from a PCR primer. Or the N-terminal of 90AA, there are residues Met-Ala that originated from PCR primer. The polypeptide of 116 AAA has both originated from PCR primer. The polypeptide of 116 AAA has both originated from a crivity and activity to binding activity Type I, type II, 312AA, 118AA, 11

Sequence 2215 BP; 778 A; 436 C; 593 G; 407 T; 0 U; 1 Other;

1960 GATAAACTTCAGACAGCTGTCCTAAAGAAACAGGGAGAAGAGAAAGGGGAACTAAAGTGCAA 1780 1601 CAGAAACGTAACAAGCAGCTAGAAGAGAAAAAAAATGCCATGCAAGAAGACAAAGATAAAA 1660 641 701 761 821 CAAGAAAGATACGAGAAAGAGAAACAGAACAGTCACCAAGTCCTACCAGAAGAATGAT 521 GAAAAGATTAAAAAGACCAAAAGAACCCAAAGAAGAAGTTAAGAGCTTCATGGATCGAAAG GAAAAGATTAAAAAGGACAAAAGAACCCAAAGAAGAAGTTAAGAGCTTCATGGATCGAAAG AAGGGATTTACAGAAGTTAAGTCGCAGAATGGAGAATTCATGACCCACAAACTTAAACAT 4 Query Match
42.3%; Score 1567; DB 2; Length 2215;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 1658; Conservative 0; Mismatches 95; Indels 4 462 1721 1781 1841 702 1901 642

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DB 4; Length 3342; T; 0 U; 0 Other;

Sequence 3342 BP; 1108 A; 590 C; 687 G; 957

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CTGCGGAATGTGTGCAGTATCTAGAAAATGAACCGTAG-TTTTGTTTTTTAAATAACAG
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Sequences AAH33071-23152 represent nucleic acid sequences derived from osteoarthrits tissues. The sequences are useful as probes and for the diagnosis or prognosis of mammalian osteoarthritis. The polymucleotides and holypeptides of the invention are useful for generating diagnostic reagents, as targets for small molecule drug development, generation of therapeutics, and cloning genes Specific antibodies are used to generate invented memosorbent assays for detection of osteoarthritis. The invented molecules can be used to treat osteoarthritis or to analyse the disease-modifying activity of osteoarthritis drugs. Other disorders treatable using the nucleic acid sequences include atopic, inflammatory and infectious disorders e.g. Crohn's disease and sepsis, and wound healing

Claim 1; Page 118-119; 144pp; English.

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Best Local Similarity 99.4%; Pred. No. 0;
Matches 1482; Conservative 0; Mismatches
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                                                 ATATCCCAGTAAACCCATGTATATTATCACTATATTTAATAATCACAGTCTAGAGATGTT
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Sequence encoding a polypeptide of human caldesmon designated type II (light) AA.
(revised)
(first entry)
25-MAR-2003
25-FEB-1993
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Homo sapiens

Caldesmon; calmodulin; actin; binding; actomysin system; regulation;

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Location/Qualifiers
12. 1607
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91JP-00089106 91JP-00358040 92EP-00302591 25-MAR-1992; EP506377-A2 30-SEP-1992

29-MAR-1991; 27-DEC-1991;

Kotani Hashida T, (SOBU/) SOBUE K. (TAKI) TAKARA SHUZO CO LID. Hayashi K, Asada K,

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WPI; 1992-325651/40.

containing that encode polypeptide of human caldesmon were selected from a containing activity and addreed by DNA sequence and the amino acid sequence encoding human caldesmon were deduced by DNA sequence analysis. Next, the inventors prepared polypeptides of various lengths, and looked for the functional domain of human caldesmon polypeptide, and looked for the functional domain of human caldesmon polypeptide, to using calmodulin-binding activity and actin-binding activity as indices. There are two forms of lower mol. Wt. is called type I and the form of lower mol. Wt. is called type II. 312AA is called type I and the form of lower mol. Wt. is called type II. 312AA and 9AA and 90AA are polypeptides that have a sequence of 116 ABs in the C-terminal portion of 118AA. I acking sequence of 312AA, and 9AA and 90AA are polypeptides that have a sequence of 118AA, there are residues Met-Ala that originated from a PCR primer. Or 118AA, there are residues Met-Ala that originated from a PCR primer. Or ilginated from a PCR primer. Or originated from a PCR primer. Or the N-terminal of 90AA, there are residues Met-Ala that originated from PCR primer. The polypeptide of 116 AAS has both calmodulin-binding activity and actin-though activity. Type II, 1312AA, 112AA, 112AA, 112AA, 112AA, 112AA, 112AA, 112AA, 113AA, 112AA, 113AA Polypeptide(s) with calmodulin- and actin binding activities - useful for treating and diagnosing cancer and regulating digestive tract motility as vasodilators. Disclosure; Page 31-32; 47pp; English

Length 2137; Sequence 2137 BP; 737 A; 424 C; 579 G; 397 T; 0 U; 0 Other; 72; Indels Score 1452.8; DB 2; Pred. No. 0; Query Match
39.2%; Score 1452.8;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 1530; Conservative 0; Mismatches

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CC conse that encode polypeptide of human caldesmon were selected from a containing the containing the containing the containing the containing the containing the containing the containing the containing calculated polypeptides of various lengths, and looked for the functional domain of human caldesmon polypeptide, and looked for the functional domain of human caldesmon polypeptide, and looked for the functional domain of human caldesmon polypeptide. There are two forms of caldesmon. Wt. is called type II. 312AA is a contained form of lower minal portion of types II. 312AA is and contained that is the C-terminal portion of types II. 312AA is and contained that is the C-terminal portion of types II. 312AA is and sequence of 312AA, and 94AA and 90AA are polypeptides that have a sequence of 116 AAS in the C-terminal contained that are in the central portion. On the N-terminal contained the N-terminal portion and the C-terminal portion. On the N-terminal contained from a PCR primer. Contained from a PCR primer. On the N-terminal of 109AA, there are residues Met-Ala that chain also contained the contained the contained the contained the contained the contained the contained the contained the contained the contained the contained contained the contained contained the contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained contained cont
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                                                                                                                                                      Sequence encoding a polypeptide of human caldesmon designated type (heavy) AA.
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Pred. No. 7.6e-244;
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               AAQ28986 standard; cDNA to mRNA; 1677 BP
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(TAKI ) TAKARA SHUZO CO LTD
                                                                                                    (revised)
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P-PSDB; AAR27363.
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Best Local Similarity
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(TAKI ) TAKARA SHUZO CO LID.
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count clones that encode polypeptide of human caldesmon were selected from a count of the calls, and the DNA sequence and the amino acid sequence encoding human caldesmon were deduced by DNA sequence analysis. Next, the inventors prepared polypeptides of various lengths, analysis. Next, the inventoral prepared polypeptides of various lengths, and looked for the functional domain of human caldesmon polypeptide.

There are two forms of caldesmon. The form of higher mol. wt. is called type I and the form of lower mol. wt. is called type II. 312AA and plypeptides that have a sequence of 116 AAS in the C-terminal portion of types I and II. 122AA and calculated the central portion of 118AA, lacking sequence of 88 AAS that are in the central portion of 118AA, lacking count the N-terminal portion and the C-terminal portion. On the N-terminal corrections of 118AA, there are residues Met-Ala that calculated from a PCR primer. Called the N-terminal of 90AA, there are residues met are residues met Ala that also criginated from a PCR primer. On the N-terminal of 122AA and 94AA, there are residues met N-terminal of 90AA, there are residues met Ala that also criginated from a PCR primer. On the N-terminal of 122AA and 94AA, there
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                                                                                                                                        GACTTGAGACCAGGAGACGTATCCAGCAAGCGGAACCTCTGGGAAAAGCAATCTGTGGAT
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are residues Met-Ala that originated from PCR primer. The polypeptide (typeI, typeII, 312AA, 122AA, 118AA, and 116AA) that contains the bolypeptide of IIG AAs has both calmodulin-binding activity and actin-binding activity. Type II, 312AA, 122AA, 118AA, 116AA all have tropomyosin-binding activity and have an inhibitory activity to actomyosin ATPASS, and have an inhibitory activity to identified as being 116AA. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
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count state that encode polypeptide of human caldesmon were selected from a cDNA library prepd. from HeLa cells, and the DNA sequence and the amino acid sequence encoding human caldesmon were deduced by DNA sequence analysis. Next, the inventors prepared polypeptides of various lengths, analysis. Next, the inventoral prepared polypeptides of various lengths, and looked for the functional domain of human caldesmon polypeptide. There are two forms of caldesmon. The form of higher mol. wt. is called type I and the form of lower mol. wt. is called type II. 312AA and 194A and 194A are polypeptides that have a sequence of 116 AAS in the C-terminal sequence of 88 AAS that are in the central portion of 118AA, lacking sequence of 88 AAS that are in the Certeminal portion. On the N-terminal continue Met-Ala that are in the Certeminal portion. On the N-terminal continue Met-Ala that are in the central portion. On the N-terminal continue Met-Ala that also and on the N-terminal of 90AA, there are residues Met-Ala that also criginated from a PCR primer. On the N-terminal of 122AA and 94AA, there
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are residues Met-Ala that originated from PCR primer. The polypeptide (typeI, typeII, 312AA, 122AA, 118AA, and 116AA, that contains the bolypeptide of 116 AAs has both calmodulin-binding activity and actin-binding activity. Type I, type II, 312AA, 122AA, 118AA, 116AA all have tropomyosin-binding activity and have an inhibitory activity to actomyosin Arpaes, and so the functional unit of human caldesmon is identified as being 116AA. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAAACCTTCTGACTTGAGACCAGGAGACGTATCCAGCAAGCGGAACCTCTGGGAAAAG
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                                                                                                                                                                                                                                           Length 939;
                                                                                                                                                                                             Seguence 939 BP; 314 A; 194 C; 275 G; 156 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                       4.
                                                                                                                                                                                                                                           Score 932.6; DB 2;
Pred. No. 5.5e-208;
                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.6%;
Matches 935; Conservative
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The present sequence is one of a large number of 5' ESTs derived from nRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. Esquences usually correspond mainly to the 3' untranalated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating CDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with inteact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. S' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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841 CCCAAACCTTCTGACTTGAGACCAGGAGACGTATCCAGCAAGCGGAACCTCTGGGAAAAG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , expressed sequence tag, secreted protein, cDNA isolation, chromosome mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 691; DB 3; Length 70 Pred. No. 1.8e-151; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 903; 71pp + Sequence Listing; English.
                                                                     CAATCTGTGGATAAGGTCACTTCCCCCACTAAGGTTTGA 2827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein 5' EST, SEQ ID NO: 903
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ilarity 99.9%;
Conservative
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                                                                                                                                                                                                                                                                                          AAC00905 standard; cDNA; 705
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P-PSDB; AAG00899.
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                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product determining the cheramination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
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Best Local Similarity 97.0%; Pred. No. 4.9e-151;
Matches 733; Conservative 0; Mismatches 20; Indels 3
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RESULT 1.
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GANGGAGGAGGAGGAAGGTCCTGGANGAGGAAGAGGAGGAAGGAACAACAGAAGGAAAG 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                 Cancer associated antigen; diagnosis; research; treatment; human;
breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
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Pred. No. 1.4e-129;
0; Mismatches 43;
                                                     CCGATCGAAACTCAGAGGAGGAAGAGAAGAGAAGA 2252
                                                                            721 ccgarcgaaaaccrrcaagaagaagaagaaga 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 67; Page 578-579; 787pp; English.
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                                                                                                                                                                                                                            Gastric cancer associated gene
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97US-0061599P.
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97US-00948705.
97GB-00021697.
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Best Local Similarity 93.1%;
Matches 647; Conservative
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                                                                                                                      RESULT 13
AAX39870/c
ID AAX39870 standard; DNA; 706
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Obata Y,
                                                                                                                                                                                                                                                                                prostate cancer; ss
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10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
22-JUN-1998;
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2576 AACATCAAGAGTATGTGGGAGAAAGGGAATGTGTTTTCATCCCCCACTGCAGCAGG----C
                        2693 CTAAC-TAAAACCCCAGATGGAAACAAGTCACCTGCTCCCAAACCTTCTGACTTGAGACC
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                                                                                                                   575 CTAACTTAAAACCCCAGATGGAAACAAGTCACCTGCTCCCAAACCTTNTGACTTGAGNCC
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                                                                                 2633 ACACCAAATAAGGAAACTGCTGGCTTGAAGGTAGGGGGTTTCTAGCCGCATCAATGG
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433 ACATCTGAAGTCAACAGAAGATCCAAGTTTAAAATTGCCTGCGGAATGTGTGCAGTATCT 492 Rosen CA Score 584.2; Claim 1; Page 2329-2330; 9803pp; English Birse CE, ВР AAH33117 standard; cDNA; 2511 28-SEP-2000; 2000WO-US026524. 99US-0163280P. 99US-0157137P. (HUMA-) HUMAN GENOME SCI INC 15.8%; (first entry) Ruben SM, Barash SC, WPI; 2001-235357/24. P-PSDB; AAG73686. WO200122920-A2. 29-SEP-1999; 03-NOV-1999; Homo sapiens 03-SEP-2001 05-APR-2001 AAH33117; Query Match 613 RESULT 15 AAH33117 ద 셤 ò 셤 ò ò AAC77607 to AAC7848 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic, proliferative, vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antidiabetic; antidiamatory; antithyroid; antialthrigic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; cocrepic; vasotropic; antipsoriatic and antiangiogenic. The noctropic; vasotropic; antipsoriatic and antiangiogenic. The present invention may be used to reat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autofimmune disorders, allergic reactions, graft versus host disease and organ crejection, modulate haemostatic or thrombolytic activity, modulate rejection, and antegonists a 3062 3122 3182 2942 3002 2882 2763 CCAGCAAGCGGAACCTCTGGGAAAAGCAATCTGTGGATAAGGTCACTTCCCCCACTAAGG 2822 ö 312 432 372 ceaecaaccegaaccrcregegaaaagcaarcreregearaagercacrrcccccccraage 132 192 252 TTTGAGACAGTTCCAGAAAGAACCCAAGCTCAAGACGCAGGACGAGCTCAGTTGTAGAGG TTTTCAATATCCCAGTAAACCCATGTATATTATCACTATATTAATAATCACTAAAA GATGTTCATGGTAAAAGTACTGCCTTTTGCACAGGAGCCTGTTTCTAAAGAAACCCATGCT 373 GIGAAATAGAGACTTTICTACTGATCATCATAACTCTGTATCTGAGCAGTGATCCAACC 3123 ACATCTGAAGTCAACAGAAGATCCAAGTTTAAAATTGCCTGCGGAATGTGTGCGAGTATCT TTTTCAATATCCCAGTAAACCCATGTATTATCACTATATTAATAATCACAGTCTAGA GTGAAATAGAGACTTTTCTACTGATCATCATAACTCTGTATCTGAGCAGTGATACCAACC 133 Trirgagacagriccagaaagaacccaagcricaagacgcagacgaggcricagricraga GCTAATTCGCTCTGTTTTGTATTTATGTTGATTTACTAAATTGGGTTCATTATCTTTAT derahirederendiringiarrianginganirachaariederiearraren 313 GAIGITCAIGGIAAAAGIACIGCCITIGCACAGGAGCCIGIIICIAAAGAAACCCAIGCI Gaps Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer. ö Score 584.2; DB 3; Length 2511; Pred. No. 3.3e-126; 0; Mismatches 8; Indels 0; Sequence 2511 BP; 814 A; 445 C; 443 G; 803 T; 0 U; 6 Other; Claim 1; Page 690-691; 2352pp; English 15.8%; ilarity 98.7%; Conservative 08-MAR-2000; 2000WO-US005882 99US-0124270P (HUMA-) HUMAN GENOME SCI INC the present invention Rosen CA, Ruben SM; 2000-587533/55. Query Match Best Local Similarity Matches 589; Conserv WPI; 2000-587533 P-PSDB; AAB43497 12-MAR-1999; 21-SEP-2000 193 253 73 2823 2883 2943 3003 3063

AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host call and culturing the cell to express the proteins. N and P can be used in the prevention diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent to publication, meaning no sequences are present for SEQ ID NO:1027 time of publication, meaning no sequences are present for SEQ ID NO:1027 3183 AGAAAAATGAACCGTAGTTTTTTTTTTTAAATACAGAAGTCATGTTGTTTCTGCACTT 3242 3243 TATAATAAAGCATGGAAGAAATTATCTTAGTAGGCAATTGTAACACTTTTTGAAAGTAAC 3302 493 AGAAAAAGGAACCGTAGTTTTTTTTTTTTAATACAGAAGTCATGTTGTTTCTGCACTT 552 Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers. Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 7; ss. Sequence 2511 BP; 814 A; 445 C; 443 G; 803 T; 0 U; 6 Other; Human colon cancer antigen encoding cDNA SEQ ID NO:173.

DB 4; Length 2511;

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Indels 0; Gaps 0;	CTTCCCCCACTAAGG 2822	criccccacrade 132	GCTCAGTTGTAGAGG 2882	Gercaerreradade 192	STICATIATCITITAT 2942	sticattarctittar 252	CTATATTTAATAATCACAGTCTAGA 3002	krádrcacácrczáca 312	CTAAAGAAACCCATGCT 3062	raabdaacccardcr 372	CTCTGTATCTGAGCAGTGATACCAACC 3122	crcigiaicidadeacidaiaceaace 432	AATGTGCAGTATCT 3182	Aargracagrarcr 492	IGTIGITICIGCACTI 3242	ndriciricidakiri 552	ACTITITGAAAGTAAC 3302	aciriridaaagraac 612		ададададте 669	
Similarity 98.7%; Pred. No. 3.3e-126; 89; Conservative 0; Mismatches 8;	2763 CCAGCAAGCGGAACCTCTGGGAAAAGCAATCTGTGGATAAGGTCACTTCCCCA	73 CGAGCAAGCGGAACCTCTGGGAAAAGCAATCTGTGGATAAGGTCACTTCCCCCACTAAGG	2823 ITTGAGACAGTTCCAGAAAGAACCCAAGCTCAAGACGCAGGACGAGCT	133 TTTGAGACAGTTCCAGAAAGAACCCAAGCTCAAGACGCAGGACGAGGTCAGTTGTAGAGG	2883 GCTAAATTCGCTCTGTTTTGTATTTATGTTGATTTACTAAATTGGGGTTCATTATCTTTTAT	193 GCIAAIICGCICIGIIIIGIAIIIAIGIIGAIIIACIAAAIIGGGIICAIIAICIIIIAI	2943 TITICAATATCCCAGTAAACCCATGTATATTATCACTATATTT	253 TITICAATATCCCAGTAAACCCATGTATATTATCACTATATTTAATAATCACAGTCTAGA	3003 GAIGITCAIGGTAAAAGTACTGCCTTTGCACAGGAGCCTGTTT	313 GAIGIICAIGGIAAAAGIACIGCCIIIGCACAGGAAGCIGIIICIAAAGAAACCCAIGCI	3063 GIGAAAIAGAGACITITICIACIGATCAICAIAACICIGIAICIC	373 GIGAAATAGAGACTTTICTACTGATCATAACTCTGTATCT	3123 ACAICTGAAGICAACAGAAGAICCAAGIITAAAAITGCCTGCGGAAIGIGTGCAGTAICT	433 ACAICTGAAGTCAACAGAAGATCCAAGTTTAAAATTGCCTGCGGAATGTGTGCAGTATCT	3183 AGAAAATGAACCGTAGTTTTTGTTTTTTAAATACAGAAGTCATGTTGTT	493 AGAAAATGAACCGTAGTTTTTTTTTTTTAATACAGAAGTCATGTTGTTTCTGCACTT	3243 TATAATAAAGGAAGGAAGAAATTATCTTAGTAGGAATTGTAACACTTTTTGAAAGTAAC	sss tataataaddatddaadaaattatcttadtagddaattotaacactttttgaaagtaac	3303 CCATITCAGATITGAAATACTGCGATAATGGTTGCTTTAAAAAAAAAA	613 CCATTTCAGATTTGAAATACTGCAATAATGGTTGTCTTTAAAA	
Best Local Matches 5	0y 2	ДQ	oy 2	qq	0y 2	Dp ·	Oy 2	υþ	9y 3	qa	3	qa	0y 3	ДQ	3	qa	δλ	Ωp	ζŏ	qq	

Search completed: March 10, 2004, 11:00:07 Job time : 916.994 secs Appli Appli Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence

ALIGNMENTS

Sequence Sequence Sequence

Sequence Sequence Sequence

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US-08-770-379-20

US-08-757-669A-20

US-08-320-371A-20

US-08-91-999-4

US-08-91-999-4

US-09-410-399-3

US-09-410-399-3

US-09-610-863-2

US-09-610-863-2

US-09-610-863-2

US-09-610-647-1

US-09-670-95-1

US-09-670-95-1

US-09-670-95-1

US-09-670-95-1

US-09-670-95-1

US-09-670-95-1

US-08-08-781A-15

US-08-08-783A-15

US-08-08-783A-15

US-08-194-088-11
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Patent No. 5532337
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Wanhington
STATE: D.C.
COUNTY: U.S.A.
STATE: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: ISM Compatible
COMPUTER: ISM Compatible
COMPUTER: ISM Compatible
COMPUTER: ISM Compatible
COMPUTER: ISM Compatible
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,440
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/858,947
FILING DATE: March 27, 1992
ATTORNEY/AGENI INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPAX:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2215 base pairs
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ORIGINAL SOURCE: Human
ORGANISM:
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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STRANDEDNESS:
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        March 10, 2004, 09:19:42 ; Search time 169.055 Seconds
(without alignments)
12152.440 Million cell updates/sec
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    /cgn2_6/ptodate/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-630-3449-113
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US-08-630-3449-112
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Listing first 45 summaries
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                                                                                                            942 ACCGAGAGGGAAGAGTTCGAGAAGCTCAAACAGAAGGAGCAGGAGGGGGCTTTGGAGCTG
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CETTION:
LIBRARY:
CONSCIPLE:
CHROMOSOME/SEGMENT:
NAME/KEY:
LOCATION:
COTHER INFORMATION: Molecular weight"
NAME/KEY:
LOCATION: 2103-2108
LIBRATIFICATION METHOD:
COTHER INFORMATION: /note= "poly A signal"
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 2099-2215
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "poly A site"
PUBLICATION INFORMATION:
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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PAGES:
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DOCUMENT NUMBER:
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GOCGCCCCCCAGGTGGAAGCCCGGCAAAAGGCTGGAGGAGCTTCGTCGTCGTCGCGGGAAG 2080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2501 ATTGAGGGAACAAAAGCGCAAAACCTACAAAGCCGGCAGCCTCGGATCTTCCTGTTCCT 2560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    702 GAAAAGATTAAAAAGGACAAAGAACCCAAAGAAGAAGAAGTTAAGAGCTTCATGGATCGAAAG
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                                                                                                                                                                                                                                                                                                                                                                 1601 CAGAAACGTAACAAGCAGCTAGAAGAAAAAAAAAACATGCCATGCAAGAGACAAAGATAAAA
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                                                                                                                                                                                                                                                     Length 2215;
                                                                                                                                                                                                                                                                                                           93; Indels
                                                                                                                                                                                                                                                        DB 1;
OTHER INFORMATION: /note= "poly A signal" FEATURE:
                                                                                                                                                                                                                                                  Query Match
42.4%; Score 1570.2;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches
                                                                                                        ; LOCATION: 2099-2215
; IDENTIFICATION METHOD:
; CTHER INFORMATION: /note= "poly A site"
US-08-630-349-14
                                                                                      NAME/KEY:
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                                   TATCTGAGCAGTGATACCAACCACATCTGAAGTCAACAGAAGATCCAAGTTTAAAATTGC 3160
                                                                                                                                                                                                                                                                                         AGTCATGTTGTTTCTGCACTTTATAATAAGCATGGAAGAAATTATCTTAGTAGGAAT
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NAME/KEY:
LOCATION: 12-1685
LOCATION: 12-1085
OTHER INFORMATION: /note= "human caldesmon of higher OTHER INFORMATION: molecular weight"
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US-08-630-349-14

ING-08-630-349-14

Sequence 14, Application US/08630349

Patent No. 573908

GENERAL INFORMATION:
APPLICANT: Ren'ichiro HAYASHI et al.
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: 105 Fifteenth Street, N.W., #700
CITY: Washington
STATE: 105 Fifteenth Street, N.W., #700
CITY: Washington
STREET: 106 Fifteenth Street, N.W., #700
COUNTRY: U.S.A.
ZIP: COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordGeriect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,349
FILING DATE: April 10, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/856,947
FILING DATE: AUGUST 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/856,947
FILING DATE: MARCH 27, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WASTERISTICS:
LENGTH: 2215 base pairs
TYPE: MUCLEIC acid
TYPE: MUCLEIC acid
TYPE: MUCLEIC acid
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MOLECULE TYPE: cDNA tO MRNA
MOLECULE TYPE: DNA
MOLECIAL SOURCE: Human
IMMEDIATE SOURCE: Hela Cell
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LOCATION: 2103-2108
IDENTIFICATION METHOD:
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FEATURE:
NAME/KEY:
LOCATION: 12-1607
LOCATION METHOD:
OTHER INFORMATION: /note= "human caldesmon of lower
OTHER INFORMATION: molecular weight"
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NAME/KEY:
LOCATION: 2025-2030
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "poly A signal"
FEATURE:
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LOCATION: 2121-2137
LOCATION METHOD:
DENTIFICATION METHOD:
OTHER INFORMATION: /note= "poly A site"
AUTHORS:
                        ZIF: 20005

COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette, 5.25 inch, 50
COMFUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,440
FILING DATE: MACH TO BATE:
APPLICATION NUMBER: 07/858,947
FILING DATE: MACH 27, 1992
ATORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REFERENCE/DOCKET NUMBER: 33.367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX:
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STRAIN:
INDIVIDIAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: Hela Cell
LIBRARY:
CLONE:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 2137 base pairs
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COUNTRY:
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                                     1362 ATTGAGGGAACAAAAAGGGGAAAACCTACAAAGGCGGGAGCCTCGGATCTTCCTGTTCCT 1421
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| Patent No. 5532337 |
| GENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: APPLICANT: CONTRESPONDENCE 32 |
| CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: STREET: Wenderoth, Lind & Ponack STREET: Wenderoth, Lind & Ponack STREET: Wanhington CITY: Washington CITY: Washington CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Application CITY: Applicati
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                                                                DB 1; Length 2137;
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                                                              Query Match 40.0%; Score 1481.6;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1548; Conservative 0; Mismatches
         FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
DOCUMENT NUMBER:
                                         S-08-285-440-13
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Patent No. 5739008

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
CORRESPONDENCES:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
CORRESPONDENCES:
CITY:
Washington
STAFET: D.C.
COUNTRY: U.S.A.
ZIP: ZOO.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 ml MEDIUM TYPE: Diskette, 3.5 inch, 144 COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,349
FILING DATE: April 10, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/285,440
FILING DATE: AUGUST 4, 1994

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1375 GGGAGAAAGGGAATGTGTTTTCATCCCCACTGCAGCAGGCACACAAATAAGGAAACTG
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                                                                                                                                           1195 CTGTGCAGAAAAGCAGTGGTGTCAAATCGACCCATCAAGCAGCAATAGTCTCCAAGATTG
                                                                                                                                                                                                                 1255 ACAGCAGACTGGAGCAGTATACCAGTGCAATTGAGGGAACAAAAGGGCAAAAACCTACAA
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    CTGAGAAACGCCAGAAGATGCCAGAAGATGGCTTGTCAGATGACAAGAAACCATTCAAGT
                           1075 CTGAGAAACGCCAGAAGATGCCAGAAGATGGCTTGTCAGATGACAGAAAACCATTCAAGT
                                                                                             CTGTGCAGAAAAGCAGTGGTGTCAAATCGACCCATCAAGCAGCAATAGTCTCCAAGATTG
                                                                                                                                                                                       2472 ACAGCAGACTGGAGCAGTATACCAGTGCAATTGAGGGAACAAAAAGCGCAAAAACCTACAA
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                                                               <u>AGCCGGCAGCCTCGGATCTTCCTGTTGAAGGTGTACGCAACATCAAGAGTATGT</u>
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                                                                                                                                                                                                                                               NAMEKEY:
LOCATION: 12-1607
LOCATION: 12-1607
LOCATION: 12-1607
LOCATION: METHOD:
OTHER INFORMATION: molecular weight"
FEATURE:
LOCATION: 2025-2030
LOCATION: 2025-2030
LOCATION: METHOD:
OTHER INFORMATION: /note= "poly A signal"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.0%; Score 1481.6; DB 1; Length Best Local Similarity 96.4%; Pred. No. 0; Matches 1548; Conservative 0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/858,947
FILING DATE: March 27, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: ADDECULE TYPE: CDNA to MRNA
ORIGINAL SOURCE: Hela Cell
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Sequence 12, Application US/08285440
Patent No. 5532337
GENERAL INFORMATION:
APPLICANT:
ATTLE OF INVENTION:
CORRESPONDENCE 32
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ADDRESSE:
CORRESPONDENCE No. 4, 700
CITY: Washington
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: D.C.
COUNTRY: U.S.A.
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MEDIUM TYPE: Diskette, 5.25 inch,
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                             SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/285,440
                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA.
PPLICATION NUMBER: 07/858,947
FILING DATE: March 27, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPHONE:
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: Hela Cell
LIBRARY:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1677 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
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PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE: Human
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DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                            COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: Display
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
STRAIN:
-08-285-440-12
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JOURNAL:
VOLUME:
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DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-285-440-12
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29.4%; Score 1087.8; DB 1; Length 1677;
Best Local Similarity 92.9%; Pred. No. 1.7e-255;
Matches 1140; Conservative 0; Mismatches 87; Indels 0;
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STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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MEDIUM TYPE: Diskette, 3.5 inch, 144 mb COMPUTER: IBM COMPATIBLE COMPUTER: IBM COMPATIBLE COMPUTER: IBM COMPATIBLE COMPUTER: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: W0/08/630,349
FILING DATE: April 10, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION NUMBER: 07/858,947
FILING DATE: MACCA 27, 1992
ATTORNEY/ABTION NUMBER: 33,367
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1677 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Patent No. 5739008
GENERAL INFORMATION:
APPLICANT: Ken'ichiro HAYASHI et
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADRRESS:
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MOLECULE TYPE: CDNA TO MRNA
ORIGINAL SOURCE: Human
IMMEDIATE SOURCE: Hela Cell
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-285-440-11
FEATURE:
NAME/KEY:
LOCATION:
LOCATION:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
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JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
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   1531 ATCAATGAATGGCTAACTAAAACCCCAGATGGAAACAAGTCACCTGCTCCCAAACCTTCT 1590
                                                            2741 GACTTGAGACCAGGAGACGTATCCAGCAAGCGAACCTCTGGGAAAAGCAATCTGTGGAT
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Fatent No. 553237
GENERAL INFORMATION:
APPLICANT:
REN'ichiro HAYASHI et al.
TITLE OF INVENTION:
POLYPEPTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
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SEQUENCE CHARACTERISTICS:
LENGTH: 1599 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE: Human
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL LINE:
CELL LINE:
CRAMSLLE:
IMMEDIATE SOURCE: Hela Cell
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POSITION IN GENOWE:
CHROMOSOME/SEGMENT:
WAP POSITION:
UNITS:
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Patent No. 5739008
GENERAL INFORMATION:
APPLICANT: Ren'inchiro HAYASHI et al.
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COUNTRY: 0.5.A.
ZIP: 20005
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Pred. No. 6.8e-234;
0; Mismatches 48;
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ORIGINAL SOURCE: Human
IMMEDIATE SOURCE: Hela Cell
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Best Local Similarity 95.5%;
Matches 1028; Conservative
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Patent No. 235237
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                                                                                Query Match 25.3%; Score 937.4; DB 1; Best Local Similarity 99.9%; Pred. No. 6.1e-219; Matches 938; Conservative 0; Mismatches 1;
              FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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  2249 AGGAGGCTAAAGGAAGAGATTGAAAGGCGAAAGAGCAGAAGCTGCTGAGAAACGCCAGAAG
                          421 Areccadadadrescrirercadareacaadadadacarricaagrerricacriceraaggr
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Sequence 295, Application US/09385982

Sequence 295, Application US/09385982

GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-06-08
BARLIER FILING DATE: 1999-06-08
BARLIER FILING DATE: 1999-01-27
BARLIER APPLICATION NUMBER: 60/117,393
BARLIER FILING DATE: 1998-01-27
BARLIER FILING DATE: 1998-01-27
BARLIER APPLICATION NUMBER: 60/098,639
BARLIER FILING DATE: 1998-01-27
SEQ ID NO 295
LENGTH: 606
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96.5%; Pred. No. 6.1e-95;
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NAME/KEY: misc feature
LOCATION: (1)...(606)
OTHER INFORMATION: n =
US-09-385-982-295
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Best Local Similarity
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US-09-385-982-295/c
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                                                    Sequence 10, Application US/08630349
Patent No. 5733008
GENERAL INFORMATION:
APPLICANT: Ken'ichiro HAYASHI et al.
TITLE OF INVENTION: POLYPEFTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOCTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,349
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 08/285,440
FILING DATE: ADULE: 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/285,440
FILING DATE: MARCH 27, 1992
ATTORNEY/AGENT INFORMATION:
NAMME: WARTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERSISTICS:
LENGTH: 939 base pairs
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STRANDEDNESS: double
TOPOLOGY: line--
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Pred. No. 4.4e-76;
0; Mismatches 2
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PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-285-440-9
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DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
CRELL LINE:
CREANTIE:
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CREANTION IN GENOME:
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MAP POSITION:
UNITS:
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NAME/KEY:
LOCATION:
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MAP POSITION:
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Best Local Similarity 99.4%;
Matches 352; Conservative
                                                                                                                      CDNA to mRNA
                          STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA to MYPOTHETICAL: ANTI-SENSE: PRAGNENT TYPE: ORIGINAL SOURCE: Human ORGANISM:
nucleic acid
                                                                                                                                                                                                                                                                                                                                                               STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                   2570 GTACGCAACATCAAGAGTATGTGGGAGAAAGGGAATGTGTTTTCATCCCCCCCACTGCAGCA 2629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 TCCCCCACTAAGGTTTGAGACAGTTCCAGAAAGAACCCAAGCTCAAGACGCAGGACGAGC 158
                                                                                                                                                                                                                                                                                                                            397 edcacacaarraaddaaacrdcrddcrrdaaddraddrrrcradcgcarcardaaa 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 TCAGTTGTAGAGGGCTAATTCGCTCTGTTTTGTATTTATGTTGATGTAATTGGGTT
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                                                                                                                                                                                                                                                      2630 GGCACACCAAATAAGGAAACTGCTGGCTTGAAGGTAGGGGTTTCTAGCCGCATCAATGAA
                                                                                                                                                              457 GTACGCAACATCCAAGAGTATGTGGNAGAAGGAATGTGTTTTCATCCCCCANTGCAGCA
        0; Gaps
        16; Indels
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APPLICANT: Ken'ichiro HAYASHI et al.
ITIE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STATE: B.C.
COUNTRY: U.S.A.
STATE: D.C.
COMPITER: B.C.
COMPITER: D.C.
COMPITER: D.C.
COMPITER: D.S.A.
ELDIN TYPE: Diskette, S.25 inch, 500 kb
COMPITER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
PLING DATE:
PLING DATE:
PRING DATE:
PRING DATE:
PRILING DATE:
PRILING DATE:
PRILING DATE:
PRILING DATE:
PRILING DATE:
PRILING DATE:
PRILING DATE:
PRILING DATE:
PRILING DATE:
REGISTRATION NUMBER: 07/858,947
PRILING DATE:
REGISTRATION NUMBER: 33,367
PRESEDENTE MAINDED:
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        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202-371-8850
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SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
             Matches 437; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2870
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US-08-285-440-8

US-08-285-440-8

Patent No. 553237

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FOLLOWITE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington
STATE: D.C.
COUWTEX: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, S.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: OF SYSTEM: MS-DOS
SOFFWARE: DisplayWitte
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
COMPUTER: ADDRESS:
FILING DATE:
FILING DATE:
COMPUTER: OF SYSTEM: MS-DOS
SOFFWARE: DisplayWitte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/858,947
FILING DATE: March 27, 1992
ATTORNEY/ABENT INROPMATION:
NAME: WARTEN W. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA to MRNA HYPOTHETICAL:
ANTI-SENSE:
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LOCATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE: Human
ORGANISM:
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STRAIN:
INDIVIDUAL ISOLATE:
DEVELOWMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: He
LIBRARY:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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FEATURE:
NAME/KEY:
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TELEX:
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                                                  GENERAL INFORMATION:
APPLICANT: Ken'ichiro HAYASHI et al.
APPLICANT: Ken'ichiro HAYASHI et al.
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: BoS Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: BM Compatible
OPERATING SYSTEM: MS-DOS
COMPUTER: BANCOMPATIBLE
OPERATING SYSTEM: MS-DOS
COMPUTER: BOTOMER: US.08/630,349
FILING DATE: April 10, 1996
CLASSIFICATION NUMBER: US/08/630,349
FILING DATE: April 10, 1996
CLASSIFICATION NUMBER: 08/285,440
FILING DATE: ADGUST 4, 1994
PRIOR APPLICATION NUMBER: 07/858,947
FILING DATE: MACHARIANO
APPLICATION NUMBER: 07/858,947
FILING DATE: MACHARATION
APPLICATION NUMBER: 33,367
INFORMATION FOR SEC ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH 369 base pairs
TYRANDENESS: double
TOOLLOWY. Innear acid
                Sequence 9, Application US/08630349
Patent No. 5739008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
MOLECULE TYPE: HUMAN
IMMEDIATE SOURCE: Hela Cell
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  US-08-630-349-9
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                                                                                                                                                                                                                                                                                                                                                             GAAAGGGAATGTGTTTTCATCCCCCCACTGCAGCAGGACACACAAATAAGGAAACTGCTGG
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                                                                                                                                 DB 1; Length 357;
                                                                                                                                 Score 350.4; DB 1; Length 3 Pred. No. 5.4e-76; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: IBM Compatible
OOFTWARE: IBM Compatible
OOFTWARE: Was Dos
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,349
FILING DATE: April 10, 1996
FILING DATE: April 10, 1996
FILING DATE: April 10, 1996
FILING DATE: August 4, 1994
PRIOR APPLICATION NUMBER: 0, 1992
ATORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 0, 1992
ATORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
SEQUENCE: ALENGTH: 357 Dase pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08630349
Patent No. 5739008
GENERAL INFORMATION:
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
) DATE:
) DOCUMENT NUMBER:
) FILING DATE:
) PUBLICATION DATE:
) RELEVANT RESIDUES IN SEQ ID NO:
US-08-285-440-8
                                                                                                                                 Query Match
Best Local Similarity 99.7%;
Matches 351; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                              Length 357;
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                                                                                                                                                                                              DB 1;
                                                                                                                                                                                           Query Match 9.5%; Score 350.4; DB 1
Best Local Similarity 99.7%; Pred. No. 5.4e-76;
Matches 351; Conservative 0; Mismatches 1
                        TOPOLOGY: linear

MOLECULE TYPE: CDNA tO MRNA
ORIGINAL SOURCE: Human

MEDIATE SOURCE: Hela Cell
US-08-630-349-8
double
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Search completed: March 11, 2004, 14:41:48 Job time : 173.055 secs

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TYPE: DNA ORGANISM: Homo sapiens
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Sequence 1815, Ap
Sequence 721, Ap
Sequence 721, Ap
Sequence 31, Appl
Sequence 31, Appl
Sequence 186, Ap
Sequence 186, Ap
Sequence 186, Ap
Sequence 187, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 183, Appl
Sequence 183, Appl
Sequence 183, Appl
Sequence 35, Appl
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(without alignments)
15799.545 Million cell updates/sec
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                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-974-289-181

5 US-10-084-817-31

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US-09-765-231A-215

US-09-925-301-100

US-09-925-301-100

US-09-974-298-183

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Sequence 9612, Ap Sequence 1194, Ap Sequence 1369, Ap Sequence 2028, App Sequence 5212, Ap Sequence 1570, Ap Sequence 50761, Ap Sequence 50761, Ap Sequence 2031, Appl Sequence 18790, Appl Sequence 18790, Appl Sequence 18790, Appl Sequence 18790, Appl Sequence 18790, Appl Sequence 18790, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequenc
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Sequence 20462, A
14 US-10-198 846-9612

14 US-10-060-036-1194

10 US-09-918-995-3028

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10 US-09-918-995-3028

10 US-09-925-301-689

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61 CATTGGCTGCCTATTAGAAAACGACAGACAATGCATACCACCGCCTCCCGACTGTAAA GCCTAGGGAATGACAGGCATCTCCACAGGCAGGCTGCATCCACTTGGCTGGGTGTCGT 61 CATTGGCTGCCTATTAGAAAAAGACAAGACAAAATGCATACCACCGCCTCCCGACTGTAAA ; DB 14; Length 3702; ; NAME/KEX: misc_feature ; CTHER INFORMATION: Incyte ID No. US20030119009A1 1312325CB1 US-10-084-817-30 1 GCCTAGGGAATGACAGGCATCTCCACAGGCAGGCTGCATCCACCTTGGC WESULT 1
US-10-084-817-30
US-10-084-817-30
Sequence 30, Application US/10084817
Publication No. US2030119009A1
Publication No. US2030119009A1
MEDICANT: Susan Stuart
APPLICANT: Jed G. Wichtern
APPLICANT: Jed G. Wichtern
APPLICANT: Jacon M. Shohet
ITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REPERRNCE: PA-0046 US
CURRENT APPLICATION NUMBER: US/10/084,817
CURRENT APPLICATION NUMBER: 60/270,784
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL PROGram
SEQ ID NO 30
LUNGTH: 3702
TVPD: NEW 0; Indels Query Match
100.0%; Score 3702;
Best Local Similarity 100.0%; Pred. No. 0;
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CRGANISM: Homo sapiens
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OTHER INFORMATION: Genbank Accession No. US20020142981A1 M83216
US-09-880-107-2406

Length 3610;

DB 9;

Score 3116.4; Pred. No. 0;

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Sequence 2406, Application US/09880107

Patent No. US20020142981A1

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf Uwe

APPLICANT: Gene Logic, Inc.

TITLE OP INVENTION: Gene Expression Profiles in Liver Cancer

TITLE OP INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERBNCE: 4921-6228-W0

CURRENT APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

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PRIOR FILING DATE: 2000-06-14

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PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SSPOTUD NO 2406

LENGTH: 3610
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APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
APPLICANT: Endrese, Gregory
APPLICANT: Endrese, Gregory
APPLICANT: Adgustus, Meena
APPLICANT: Carter, Renneh
APPLICANT: Carter, Renneh
APPLICANT: Carter, Renneh
TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION: Signature Gene Sets
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR PILING DATE: 2000-09-29
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
SETON APPLICATION NUMBER: U.S. 60/244,867
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 1067
SOFTWARE: Patentin version 3.0
SEQ ID NO 721
LENGTH: 3610
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                                                                            Sequence 721, Application US/09873367C Publication No. US20030165839A1 GENERAL INFORMATION:
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Matches 3140; Conservative
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7 OTHER INFORMATION: a, t, c,

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; OTHER INFORMATION: Incyte ID No. US20020156263A1 022404.25
US-09-974-298-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/09974298
Patent No. US20020156263A1
Facent No. US20020156263A1
FAPLICANT: Chen, Huel-Mei
FILE REFERENCE: PA-0037
FILE REFERENCE: PA-0037
FILE REFERENCE: 2001-10-04
FILE REPERENCE: 2001-10-04
FRIOR FILING DATE: 2001-10-04
FRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 36
LENGTH: 4547
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 76.9%;
Matches 2585; Conservative
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ORGANISM: Homo sapiens
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US-09-974-298-36
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IITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS FILE REFERENCE: PA - 0026-1 CTP
CURRENT APPLICATION NUMBER: US 10/062,674
CURRENT FILING DATE: 2002-01-30
PRIOR FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 2217
SOFTWARE: PERL PROGRAM
SEQ ID NO 1816
LENGTH: 4261
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47.8%; Score 1771; DB 15; Length 4261;
Best Local Similarity 76.7%; Pred. No. 0;
Matches 2578; Conservative 0; Mismatches 16; Indels 768; Gaps
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ORGANISM: Homo sapiens
PRATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040005559A1 256147.57
PRATURE:
NAME/KEY: unsure
LOCATION: (1) ... (4261)
COTHER INFORMATION: a, t, c, g, or other
US-10-062-674-1816
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US-10-062-674-1816
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                                             1800 AAGAAGACAAGCCTACCTTCAAAAAAGAAGAGATCAAAGATGAAAAGATTAAAAAGGACA
                                                                                 AGTCGCAGAATGGAGAATTCATGACCCACAAACTTAAACATACTGAGAATACTTTCAGCC
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                                     GAAACCATTCAAGTGTTTCACTCCTAAAGGTTCATCTCTCAAGATAGAAGAGGAGCAGA
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US-10-341-434-136

SGUENCE 136, Application US/10341434

SEQUENCE 136, Application US/10341434

Publication No. US20030215835A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1

CURRENT PAPLICATION NUMBER: US/10/341,434

CURRENT FILING DATE: 2003-01-18

PRIOR APPLICATION NUMBER: US 60/348,119

PRIOR APPLICATION NUMBER: US 60/348,119

PRIOR FILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 238

SOFTWARE: Patentin version 3.1

LENGTH: 2845 Length 2845; Indels 0; Mismatches 20; DB 15; Score 1578; Pred. No. 0; Query Match
Best Local Similarity 75.1%;
Matches 2376; Conservative ; NAME/KEY: CDS ; LOCATION: (230)..(1843) ; OTHER INFORMATION: US-10-341-434-136 TYPE: DNA ORGANISM: Homo sapiens

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                                                                       TCTGTATCTGAGCAGTGATACCAACCACATCTGAAGTCCAACAGAAGATCCAAGTTTAAAA
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Sequence 215, Application US/10341434

Publication No. US20030215835A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
TITLE OF INVENTION: US 00140-18

CURRENT APPLICATION NUMBER: US/10/341,434

CURRENT FILING DATE: 2002-01-18

PRIOR PILING DATE: 2002-01-15

PRIOR PILING DATE: 2002-01-15

NUMBER OF SEQ ID NOS: 238

SOFTWARE: Patentin version 3.1

SEQ ID NO 215
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Pred. No. 0;
0; Mismatches 20; Indels 766;
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Best Local Similarity 75.1%;
Matches 2376; Conservative
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; LOCATION: (230)..(1843)
; OTHER INVENTION:
US-10-341-434-215
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OY 2677 CCGCATCAATGAATGGCTAACTAAAACCCCAGATGGAAACTCACCTGCTCCCAAACC 2736 1696 CCGCATCAATGAATGGCTAACTAAAACCCCAGATGGAAACAAGTCACCTGCTCCCCAAACC 2736 2737 TTCTGACTTGAGACCAGAGACCTATCCAGCAAGCGAACCTTCTGGGAAAACCATCTTC 7796 Db 1756 TTCTGACTTGAGACCAGAGACCTATCCAGCAAACCAACTCTGT 2796 2737 GGATAAGGTCACTTCCCCCCATTGAGACCTTCAGGAAAAGAACAATCTGT 1815 Db 1756 GGATAAGGTCACTTCCCCCACTAAGGTTTGAGACAGAAAGAA	2857 ACCCAGACCACTCATTGTAGACCCTAATTCGTCTGTTTTTTTT	APPLICANT: Dotson, Stanton APPLICANT: Dotson, Stanton APPLICANT: Dotson, Stanton APPLICANT: Ma, Xiao-Jun TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides, TITLE OF INVENTION: Vectors, and cells FILE REFERENCE: 50-3221 PR CURRENT APPLICATION NUMBER: US/09/765,231A CURRENT FILING DATE: 2001-01-18 NUMBER OF SEQ ID NOS: 82 SEQ ID NOS: 82 IENGTH: 3342 TYPE: DNA CRGANISM: Homo sapiens US-09-765-231A-32 Query Match 39.3%; Score 1455.8; DB 9; Length 3342;
GAGCAGAAACGTAACAAGCAGCTAGAAGAAAAAAACATGCCATGCAAGAGATAAATGAAAGAT AAAGGGGAAAAAGGTAGAACAGAAAATAGAAGGGAAATGGGTAAATGAAAAGAAAG	1777 GCAGCTAAAAGAGAAAAAGACCCAAAGAAGATTAAAAAGAGATTAA 1836 1899	2437 ATGGACCCATCAAGGAGAATAGTCTCCAAGATTGACAGCAGACTGGAGGAGTATACCAG 2496 1456 ATGGACCCATCAAGGAGCAATAGTCTCCAAGATTGACAGCAGACTGGAGGAGTATACCAG 1515 2497 TGCAATTGAGGGAACAAAAGCTCCAAAACTTCAAAGCCGGCAGCTCGGATCTTCCTGT 2556 1516 TGCAATTGAGGGAACAAAAACCTACAAAGCCGGCAGCCTCGGATCTTCCTGT 1575 2557 TCCTGCTGAAGGTGAAGAAAACCTACAAAGCGGAGAGCTTCCTGT 1575 2557 TCCTGCTGAAGGTGAAGAAACTAAAAGGAAAACGGAAAAGGAGAAAAGGAAAACGTTTCATC 2616 1576 TCCTGCTGAAGGTGAAGAAACTAAAAGGAAAAAAAAAAA

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US-09-974-298-35
US-09-974-298-35
Sequence 35, Application US/09974298
Sequence 35, Application US/09974298
Sequence 36, Application US/09974298
SEMERAL INFORMATION:
APPLICANT: Chen, Huei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
SPIOR PILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                       DB 14;
                                                                                                                                                                                                                                                                                       Query Match
15.8%; Score 584.2; DB 14
Best Local Similarity 98.7%; Pred. No. 1.8e-138;
Matches 589; Conservative 0; Mismatches 8;
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               COCATION: (44)...(44)
COCHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (2456)...(2456)
COTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (2488)..(2488)
COCATION: (2488)...(2488)
COCATION: (2488)...(2488)
COCATION: (25188)...(2511)
COCATION: (2511)...(2511)
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COCATION: (2511)...(2511)
COCATION: (2511)...(2511)
NAME/KEY: misc_feature
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APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polymucleotides and Polypeptide FILE REPERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT FILING DATE: 2002-03-28

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8664

SOFTWARE: Patentin Ver. 3.0

SEQ ID NO 183
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                                                                                                                                                2823 TITGAGACAGTICCAGAAAGAACCCAAGCICAAGACGCAGGAGGTCAGTIGTAGAGG 2882
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                                                               2763 CCAGCAAGCGGAACCTCTGGGAAAAGCAATCTGTGGATAAGGTCACTTCCCCCACTAAGG
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                      0; Gaps
                      Indels
  Pred. No. 1.8e-138;
0; Mismatches 8;
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Publication No. US20030109690A1
GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
NAME,KEY: misc_feature
LOCATION: (28)

OTHER INFORMATION: n equals a,t,g,
98.7%;
Best Local Similarity 98.7
Matches 589; Conservative
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ORGANISM: Homo sapiens
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Sequence 16172, Application US/10085783A

Publication No. US20040037841A1

GENERAL INFORMATION:

APPLICANT: Chondrodene Inc.

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

LENGTH: 541

LENGTH: 541
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    3228 GTTGTTTCTGCACTTTATAATAAGCATGGAAGAAATTATCTTAGTAGGCAATTGTAACA 3287
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                                                                                        CITITIGAAAGTAACCCATITICAGATITIGAAATACTGCGATAATGGTTGCTTTAAAAAA
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                                         GTTGTTTCTGCACTTTATAATAAGCATGGAAGAAATTATCTTAGTAGGC-ATTGTAACA
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llarity 96.2%; Pred. No. 4.1e-117;
Conservative 0; Mismatches 20;
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511; Conserv
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; ORGANISM: Human
US-10-085-783A-16172
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Best Local S
Matches 511
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                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                          Indels 217;
                                                                                                                                                                                                   Length 2209;
                                                                                                      NAME/KOY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 022404.23
US-09-974-298-35
                                                                                                                                                                                              Score 546.8; DB 9;
Pred. No. 6.2e-129;
0; Mismatches 7;
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                                                                                                                                                                                              Query Match
Best Local Similarity 78.3%;
Matches 808; Conservative
SEQ ID NO 35
LENGTH: 2209
TYPE: DNA
ORGANISM: Homo sapiens
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